

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2005, 20:12:33 ; Search time 19 Seconds
(without alignments)
2643.429 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLVRLKRTWPLEVPETE.....DRFPFRSGRPTDGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	8.7	475	2 A86372	53.0K hypothetical
2	187.5	6.8	350	2 H86371	40.0K hypothetical
3	145.5	5.3	547	2 T46366	hypothetical prote
4	128.5	4.7	842	2 T32258	hypothetical prote
5	118	4.3	564	2 H70804	hypothetical prote
6	117.5	4.3	1213	2 A41724	limb deformity (ld
7	117	4.2	403	2 S52796	prp12 protein - hu
8	116.5	4.2	915	2 T12526	hypothetical prote
9	116	4.2	4957	2 T03455	ALR protein - huma
10	116	4.2	5262	2 T03454	ALR protein - huma
11	112	4.1	1006	2 G86292	hypothetical prote
12	111.5	4.0	940	2 JE0291	FB19 protein - hum
13	111	4.0	1097	2 T49187	hypothetical prote
14	110.5	4.0	551	2 S57447	HPBII-7 protein -
15	110	4.0	424	2 A54964	spliceosome-associ
16	110	4.0	1468	2 S11515	formin - mouse
17	109.5	4.0	742	2 A49672	transcription fact
18	109.5	4.0	772	2 A55004	transcription fact
19	109	4.0	741	2 I48694	probable transcrip
20	109	4.0	1206	2 S24407	formin isoform IV
21	109	4.0	2783	1 A1948	alpha-fetoprotein
22	108	3.9	311	2 T15997	hypothetical prote
23	108	3.9	577	2 T09024	proline-rich prote
24	107.5	3.9	589	2 T29299	hypothetical prote
25	107	3.9	351	1 JSBYP1	centromere-binding
26	107	3.9	505	2 A53152	annexin XI - human
27	107	3.9	1257	2 T01020	hypothetical prote
28	106.5	3.9	212	2 S57330	cathelin-like anti
29	106.5	3.9	584	2 G71676	hypothetical prote

RESULT 1
A86372
53.0K hypothetical protein F508.33 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86372
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86372
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <STO>
A:Cross-references: UNIPROT:Q9ZUB8; GB:AE005172; NID:G4056460; PIDN:AAC98033.1; GSPDB:GM C:Genetics:
A:Map position: 1

ALIGNMENTS

Query Match	8.7%	Score 240.5	DB 2	Length 475
Best Local Similarity	24.5%	Pred. No. 1.2e-09		
Matches 116	Conservative 89	Mismatches 177	Indels 91	Gaps 20
QY	1 MRLVRLKRTWPLEVPETEPTLGLHRLSHRLSLCTGCGYSSNTFRITITLYKDPL--TG 58			
Db	3 LRLRHETRETLEKLADAD-TLHDLRRINFTV-----PSSVHLSLNKRDELITPS 53			
QY	59 DEETLASVIGSDLICILQDDIPAPNPSTDSHSLQNEQPSLATSSNOTSMQDE 118			
Db	54 PBDTLRLSLIGDLIYFSLE-----AGESNNWKLKRDSETVASQESNOTSVHD- 102			
QY	119 QSDSDFQQAQSGVWNDDSLGPSQNFPEISIQNAHAE--TGFYFSEPM----- 169			
Db	103 --SIGF---AEVDVPPDQAKSNPN-----TSVED-----PEGDISGMEPEPMDEQLDM 147			
QY	170 --LCSESVEGVPHSLIET--LYQSADCSANDALIVLIHLLMLESGYI--PQOTE----- 218			
Db	148 ELAAGSKSLSPFFFLKNILLEKSGDTSLELT-TLALSVAHVLMLESGFVLLNHGSKDFNFS 206			
QY	219 AKALSNPEKWLKSGVYKQYMHPLCEGGSATITCVPLGNLIVVNATL-----KINNEI-- 271			
Db	207 KELLATVSLRYTLPELIKSKDNTI---ESVSKVQNLGPVWVYGVTVGSSGRVHVNLDK 263			
QY	272 -RSVKRLQLPESFCICEKLGENVANIYKDLQKLSLFDQLVYPLLATRQALNLPDVF 330			
Db	264 RRFVPVIDLVMDTSTSDSDE---EGSSSIYREVFMFWRNVKDRVLVPLLIIGICDKAGLEPPP 320			

proline-rich prote
hypothetical prote
hypothetical prote
spindle pole body-
beta-galactosidase
chromodomain helic
Wiskott-Aldrich sy
protein F20824.6 l
hypothetical prote
hybrid proline-ric
ras GTPase-activat
probable integral
proline-rich prote
probable transcrip
hypothetical prote
probable type II D

[illegible]

RESULT 2

H86371
40 OK hypothetical protein F508.32 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86371
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ensen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86371
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <STO>
A:Cross-references: UNIPROT:Q9ZUB9; GB:AE005172; NID:G4056459; PIDN:AAC98032.1; GSPDB:GN
C:Genetics:
A:Map position: 1

RESULT 3
T46366
hypothetical protein DKFZp434C0118.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence revision 04-Feb-2000 #text change 09-Jul-2004

C;Accession: T46366
R;Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: 223031
A;Accession: T46366
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-547 <AAA>
A;Cross-references: UNIPROT:Q9NT57; EMBL:AL137520
A;Experimental source: adult testis; clone DKFZp434C0118
C;Genetics:
A;Note: DKFZp434C0118.1

RESULT 4

T32258
hypothetical protein C24A1.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32258
R:Connell, M.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid C24A1.
A:Reference number: Z21141
A:Accession: T32258
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-842 <CON>
A:Cross-references: UNIPROT:O17055; EMBL:AF024491; PIDN:AAB70312.1; GSPDB:G
A:Experimental source: strain Bristol N2; clone C24A1
C:Genetics:
A:Gene: CESP:C24A1.3
A:Map position: 3
A:Introns: 43/2; 189/3; 234/1; 351/1; 511/3; 578/3; 594/2; 636/2; 675/3
Query Match 4.7%; Score 128.5; DB 2; Length 842;
Best Local Similarity 20.3%; Pred. No. 0.35;

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Matches 109; Conservative 79; Mismatches 197; Indels 151; Gaps 25;
QY 14 LEVPEPTGLHRLSHRLSLCTWGYSSNTFTITLNYKDLPTGDEETLASVIGVSGDL 73
D 14 LEVPEPTGLHRLSHRLSLCTWGYSSNTFTITLNYKDLPTGDEETLASVIGVSGDL 73
D 334 MKYPGVDPNYQDGHGTHALSHCYHGLRIVGYLLE-----NGAQSLASRAPEGGAL 386
QY 74 ICLILQDDIPAPNIPSSSTSEHSSQNNQPSLSTSSNOTSMQDQPSDFQQAQSGV 133
D 74 ICLILQDDIPAPNIPSSSTSEHSSQNNQPSLSTSSNOTSMQDQPSDFQQAQSGV 133
D 387 ----RQAAGPCTNRPSKVASAIMALNRSSTPSNASTVSLDDQQTPTV-----I 433
QY 134 W-----NDDSMGLPSONFEAESIQDNAHMAEGTGFPEPMLCSESVEGO-----VPHSLE 184
D 134 W-----NDDSMGLPSONFEAESIQDNAHMAEGTGFPEPMLCSESVEGO-----VPHSLE 184
D 434 WAYERGHDAIVALLKHYAARTVEGD-----VCSEYSSGESSYTPLPSPMG 478
QY 185 TL-----YQASCDSDANDALIVILHLMESGY-----IPQTEAKALSMPEKWLKSGVYKQ 237
D 185 TL-----YQASCDSDANDALIVILHLMESGY-----IPQTEAKALSMPEKWLKSGVYKQ 237
D 479 RLTSRLTRDADLLQLRSALPAPFHLCLABIEFQESIGSGSGFGK-----VYKGT 526
QY 238 YMHPLCEGSSATLCTVPLGNLIVVNATLKNINNEIRSVKELQLLPSPFICKELGENVANI 297
D 238 YMHPLCEGSSATLCTVPLGNLIVVNATLKNINNEIRSVKELQLLPSPFICKELGENVANI 297
D 527 YR-----GKLV-----AVKRYRAM--AFGCKSE-----TMDL 551
QY 298 YKDLQKLSRLFKDQLVPLPLATFROALNLPDVGLVPLPLEL-----KLRIPLRLD 348
D 298 YKDLQKLSRLFKDQLVPLPLATFROALNLPDVGLVPLPLEL-----KLRIPLRLD 348
D 552 CREVSTLSLAPNVV---AFVGTSLDPSQFAITFEVNGSLFRRENGERKRYRVD 607
QY 349 ----VRSVLSSAVCRDLFTASNDPLLMRFL-----VLRDFRDNTRVQDPT 391
D 349 ----VRSVLSSAVCRDLFTASNDPLLMRFL-----VLRDFRDNTRVQDPT 391
D 608 PAFRLRLSLDVARGMYLHESAAPVIHRLDLSHNLIIHADGRSVVADFGESRFVQCRD 667
QY 392 WKELRYKRIHQKESPK-----GRFVMLLPSTHTIIPFPNPLHPRPPSPSLRPGIIG 446
D 392 WKELRYKRIHQKESPK-----GRFVMLLPSTHTIIPFPNPLHPRPPSPSLRPGIIG 446
D 668 -ENLTQPGNLRWMAPEVFSQSGKYDRKVDVFSFALVIW--EHTAELPFSHLKPAASAAA 724
QY 447 E--YDQ-RPTLPVGGDP-----ISSLPFGCETPSQFPPLRPRFDPVGPPLGPN 492
D 447 E--YDQ-RPTLPVGGDP-----ISSLPFGCETPSQFPPLRPRFDPVGPPLGPN 492
D 725 ENTYKGRITLP--NQPTAQFPAHLISLILPOAWHPRESS---SRPDEIVEIVALLEPH 775

RESULT 5
H70804
Hypothetical protein Rv3494c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: H70804
R:Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: H70804
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-564 <COL>
A:Cross-references: UNIPROT:053539; GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAAL1773
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3494c

Query Match 4.3%; Score 118; DB 2; Length 564;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 51; Conservative 18; Mismatches 51; Indels 80; Gaps 11;
QY 354 SLSAVCRDLF--TASNDPLLMRFLYLRDFRDNTRV--VQDWMKELYRKR--HIQKESPK 408
D 354 SLSAVCRDLF--TASNDPLLMRFLYLRDFRDNTRV--VQDWMKELYRKR--HIQKESPK 408
D 343 SVREIPRDMYCKTAQNDP-----STVRGARNYPCQEPFGKRAPTVQLCRDRP 389
QY 409 GRFVMLLPSTH--TIPTFP-----NPLHPRFPSPSLRPPGIIIGYDQRTPLPV 457
D 409 GRFVMLLPSTH--TIPTFP-----NPLHPRFPSPSLRPPGIIIGYDQRTPLPV 457
D 390 G-----YVPVGTNWRGPPPIPYGTEVTDGRNLIIPNKKFP--YIPPGA-----DPDQGVPIV 438
```

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QY 458 GDPISSLIPGCGETPSQ-----PPPLRPRF-----PPPLRPRF----- 482
D 439 GPPPPGQVAGCPGAPQHPAQAPAPPNDNGPPPPFTSMWPPGYPPEPPQVYPATIPPPPP 498
QY 483 -----DPVGPLPGPNPILPG 497
D 499 PEGTGPFPGPAGPQPOQASG 518

RESULT 6
A41724
limb deformity (ld) protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 04-Mar-1993 #sequence_revision 15-Aug-1997 #text_change 09-Jul-2004
C:Accession: S24286; S38780; A41724
R:Trump, A.; Blundell, P.A.; de la Pompa, J.L.; Zeller, R.
Genes Dev. 6, 14-28, 1992
A:Title: The chicken limb deformity gene encodes nuclear proteins expressed in specific
A:Reference number: A41724; MUID:92112031; PMID:1730407
A:Accession: S24286
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1213 <TRU>
A:Cross-references: UNIPROT:Q05858; EMBL:X62681
A:Experimental source: embryo
R:Zeller, R.
submitted to the EMBL Data Library, August 1991
A:Reference number: S38780
A:Accession: S38780
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-885, 'A', 887-1213 <ZEL>
A:Cross-references: EMBL:X62681; NID:g63567; PID:g63568
C:Comment: Mutations in this gene affect morphogenesis of both limbs and kidneys.
C:Genetics:
A:Gene: ld
C:Keywords: nucleus

Query Match 4.3%; Score 117.5; DB 2; Length 1213;
Best Local Similarity 19.4%; Pred. No. 3.7;
Matches 105; Conservative 55; Mismatches 204; Indels 177; Gaps 19;
QY 57 TCDEETLASVIGVGDLCILQDDIPAPNIPSSSTSEHSSQNNQPSLSTSSN----- 111
D 297 TEDGETITEIKPRENDLALLKLRQPVKSNITSLGTTKKKSEPKASPTFLQLSHLLMI 356
QY 112 QTSMDQEPSDSFOGQAQSGVWDDSLMGPSONFEAESIQDNAHMAEGTGFVPSPEMLC 171
D 357 DVSKNDERTDQSCAGFGE-----TEDSGEPENKASGQ-----TEPLFP 395
QY 172 SESVEGQVPHSLLETLYQSADCSANDALIVLILHL-----MLSEGYIPQGTGA-KALSMPE 226
D 396 SBEIKS-----SPAESALDVFKALFTRPPKETTADPSELEAIKRWNE 440
QY 227 KWLSGVYKLYQMHPLCEGSSATLCTVPL-----GNLIVVNATLKNINNEIRSVKRLQL 279
D 441 KESLKAVERFSKSGKDGPSDKSPDLSFSEQDDKTFGRQLQTVWPPPKANHE----- 491
QY 280 LPESFICKELGENVANIYKDLQKLSRLFKDQLVPLPLATFROALNLPDVGLVPLPLEL 339
D 492 -----EVKVGKLYTEAEYQAAILHLKREHKE-----IETLKSQF 526
QY 340 KLRIPLRLDVRSVLSL-----SAVCRDLFTASND---PLLWRFY 376
D 527 ELRVPHIRGEHAVSTAQLEETIAHLKNELDKLNLRNEEARDIGVSTEDDNLPKTYRNV 586
QY 377 LRDFRDNTRVQDWMKELYRKRHIQKESPKGRFVMLLPSTHTI----- 422
D 587 IOTDRETFIKPSEENRAVKNQIVPKK-----LNISSLTHSISTQGENKDSVDPS 638
QY 423 -----PFYNNPLHPRFPSPSLRPPGIIIGYDQRTPLPVYGDPISSLIP-- 466
D 639 SESVLSCQPKQMLPPSPPPPPPPPPPP-----PP-----PPPPFSDSLFGLVPP 684
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Qy 467 -----GPGETPSQF---PPLRPRF-----DPVGPPLPGNPPLPGRCGGPNDRPFRPSRGR 513
 Db 685 PPLPTGPTSVTHFAFGPPLPQLSEGCGRDFOAPPAPPPPLPGLGPPVP--PPLPGSGL 742
 Qy 514 P 514
 Db 743 P 743

```

RESULT 7
S52796
  prp12 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 10-Nov-1995 #text_change 10-Sep-1997
C:Accession: S52796
R:Ruhlmann, A.; Kreideweiss, S.; Nordheim, A.
  submitted to the EMBL Data Library, March 1995
A:Reference number: S52796
A:Accession: S52796
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <RUH>
A:Cross-references: EMBL:X86019; NID:g762950; PID:g762351

```

```

RESULT 8
T12526
hypothetical protein DKFZp434M183.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T125236
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Cassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence database, June 1999
A:Reference number: Z17524
A:Accession: T12526
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-315 <WAM>
A:Cross-references: UNIPROT:Q9Y4Q8; EMBL:AL080141
A:Experimental source: adult testis; clone DKFZp434M183
C:Genetics:
A:Note: DKFZp434M183.1

```

Db	308	LLGELGPAVELCLKEERFADAILLAQAAGTDLLKQTERYVLAKKKT--KISSLLACVVQK	365
Qy	190	-----ADCS DAN--DALIVLHLLMESGYIPQGTAKALSMPERKWKLVGVYKLOYMHP	241
Db	366	NWKDVVCTCSLKNWREALALLTY-----SGTE---KPELCDMLGTRMEQ----	408
Qy	242	LCGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICK---EKLGENVANIY	298
Db	409	--EGSRA-----LTSEARL-----CYVCSGSVERLVECWAKCH	439
Qy	299	KDLQKLRLFKDLQVYPLLAFTROALNLPDVGLVVLPLELKLRIIFRLLDVRSVL----	353
Db	440	--QALSFWALQDLMEKVMVLRNLSLEQLRGPHGVSGP-----ATTYRVTQYANLLAAGS	492
Qy	354	--SLSAVCRD-----LFTASNDPILLWR-----FLYLRDFRDNTVRVQDITWKE	394
Db	493	LATAMSFILPRCAQPPVQOQLRDLRFLHAQGS AVLGOQSPFPFPFRIVVGVTLHSGKETSYR	552
Qy	395	L-YRKRHHIQRKESPKGRFVMLLPSSHTTIPFVNPPLHPRPPSSR-----	438
Db	553	LGSQPSHQVPTSPRPR--VFTPQSGSPAMPLAPS--HPSFYQGPRTQNI SDYRAPGPQAI	608
Qy	439	----LPPGI-----IGGYDQRP-----TLPYVVDGPISSLIPG---PG-----E	470
Db	609	QPLPLSPGVRPASSQPQLLGGQRVQVPNPVGPFGTWP LPGSPPLMACPGIMRPGSTSLPE	668
Qy	471	TPSOFP--PLRP-----RDPDVGPLGPNPILPG-----RGGPND	503
Db	569	TPRLFLPLPLRLPGRMVSHTPAPSPAPFVYLPDGPAGCSSVLPTTGILIPHGPQD	728
Qy	504	RFPFRPS-RGRPTDGRL--SPM	522
Db	729	SWKEAPAPRGNLQRNKLPETFM	750
RESULT 9			
T03455			
ALR protein - human			
C:Species: Homo sapiens (man)			
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004			
C:Accession: T03455			
R:Prasad, R.; Zhadanov, A.B.; Sedkov, V.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997			
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homology			
A:Reference number: Z14954; PMID:97388474; PMID:9247308			
A:Accession: T03455			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-4957 <PRA>			
A:Cross-references: UNIPROT:O14686; EMBL:AF010404; NID:G2358286; PIDN:AAC51735.1; PID:G2358286			
C:Genetics:			
A:Gene: ALR			
A:Map position: 12			
C:Superfamily: acute lymphoblastic leukemia protein, ALR type			
C:Keywords: alternative splicing			

	Query Match	4.2%;	Score 116;	DB 2;	Length 4957;	
	Best Local Similarity	20.0%;	Pred. No. 37;			
	Matches 102; Conservative	64;	Mismatches 181;	Indels 164;	Gaps 25;	
Qy	94 EHSLSQNNNEOPSLSATSSNTSMODEPDSDFOCQAQS--GVNDD-SMLGSPQNFEAES	150				
	: :					
Dd	3356 QQQQLQOQQQQQLQOQQQQQLQOQQQQQQQQQFQOQQQQQGLLNQRTLLSPOO----	3409				
	: :					
Qy	151 IQDNAHMAECTGFVPSEPMM-----LCSESVE-----	176				
	: :					
Dd	3410 -QQQQVALGPGM-PAKPLQHFFSPGALGPLTLLTGKEQNTVDPAVSSSEATEGFSSTHQGG	3467				
Qy	177 -----GOVPHSLETYOSADCSNDANDALIIVLIHLMLLESYIPO-GTEAKALSMPERKWKL	231				
	: :					
Dd	3468 PLAIGTTPESMATPEGEVKPSLGSDSLIIAQV-----POPQPSSLOQPPLURLP	3518				
	: :					

```
QY 232 GYKIQ--YMH-----PLCEGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLP 281
Db 3519 GQQQQVSLHTTAGGSHGQLGSSSEASSVP---HLLAQPSVSLGDPGQSGMTQNLILGP 3575
QY 282 ESFICKEKLGENVANIYKDLQKLSLRFKDQLVYVLLAFTRQALNLPDVFGLVVLPLELKL 341
Db 3576 QQPMLEPQNNTGP-----QPPKPGVL---QSCQGLP---GVCIMTVGQL 3617
QY 342 RIFRLDVRSLVLSAVCRDLFTASNDPLLWFLYLRDRFRONTVRVQDTWKELYRKHI 401
Db 3618 R-----AQLQGVLAKNPQLRHLSPOQQQL-----QALLMQRQL 3651
QY 402 QKESPKGRFVMLLP-----SSTHTIPF-----YNP-----LHPRPPFS 436
Db 3652 QOSQA-----VRQTPPYQEPGTQTSPLQGLLCCQPLGCGFPQTGQLQELGAGRPQGP 3706
QY 437 SRL--PPGIIGGEYDQRTPLPVVG-----DPISLLIPGGETPSPFPPLRPFRDVGPLP 489
Db 3707 PRLPAPPGALS-----TGPVLGPHVHTPPSS--POEPKRPSPQLPSSSQLPTEAQLP 3757
QY 490 GNPILPGRGGPNDRFPPRPSRGRPTDGRLS 520
Db 3758 PTHPGTPKPGQPTLEPP--PGRVSPAAQA 3786

RESULT 10
T03454
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03454
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano,
Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homology
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03454
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5262 <PRA>
A:Cross-references: UNIPROT:O14686; EMBL:AF010403; NID:g2358284; PIDN:AACS1734.1; PID:g2
C:Superfamily: acute lymphoblastic leukemia protein, ALR type
C:Keywords: alternative splicing

Query Match 4.2%; Score 116; DB 2; Length 5262;
Best Local Similarity 20.0%; Pred. No. 41;
Matches 102; Conservative 64; Mismatches 181; Indels 164; Gaps 25;

QY 94 BHSLLQNNNEQPSLATSSNQTSMDQPSDSFOGQAQS--GVWDD-SMLGPSQNFSAES 150
Db 3661 QQQQLQQQQQQQLQQQQQQQLQQQQQQQQQQQQQQQQQQQQQQGMLLNQSRLLSPQQ----- 3714
QY 151 IQDNAHMAEGTFYPSSEPM-----LCSESVE----- 176
Db 3715 -QQQQQVALPGM-PAKPLQHFSSPCALGPTLLATGKEQNTVDPASVSEATGEPSTHQGG 3772
QY 177 ----QGVHSLLETLQSDACSDANALIVLHLLMESGYIPO-GTEAKALSMPEKWLK 231
Db 3773 PLAIGTTPESMATEPGEVKPVSUGSDQLLLVQ-----POQOPSSQLQPLPLP 3823
QY 232 GYKIQ--YMH-----PLCEGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLP 281
Db 3824 GQQQQVSLHTTAGGSHGQLGSSSEASSVP---HLLAQPSVSLGDPGQSGMTQNLILGP 3880
QY 282 ESFICKEKLGENVANIYKDLQKLSLRFKDQLVYVLLAFTRQALNLPDVFGLVVLPLELKL 341
Db 3881 QQPMLEPQNNTGP-----QPPKPGVL---QSCQGLP---GVCIMTVGQL 3922
QY 342 RIFRLDVRSLVLSAVCRDLFTASNDPLLWFLYLRDRFRONTVRVQDTWKELYRKHI 401
Db 3923 R-----AQLQGVLAKNPQLRHLSPOQQQL-----QALLMQRQL 3956
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QY 402 QKESPKGRFVMLLP-----SSTHTIPF-----YNP-----LHPRPPFS 436
Db 3957 QOSQA-----VRQTPPYQEPGTQTSPLQGLLCCQPLGCGFPQTGQLQELGAGRPQGP 4011
QY 437 SRL--PPGIIGGEYDQRTPLPVVG-----DPISLLIPGGETPSPFPPLRPFRDVGPLP 489
Db 4012 PRLPAPPGALS-----TGPVLGPHVHTPPSS--POEPKRPSPQLPSSSQLPTEAQLP 4062
QY 490 GNPILPGRGGPNDRFPPRPSRGRPTDGRLS 520
Db 4063 PTHPGTPKPGQPTLEPP--PGRVSPAAQA 4091

RESULT 11
G86292
hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86292
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroo, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86292
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1006 <STO>
A:Cross-references: UNIPROT:O9LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN
C:Genetics:
A:Map position: 1

Query Match 4.1%; Score 112; DB 2; Length 1006;
Best Local Similarity 32.7%; Pred. No. 7;
Matches 36; Conservative 6; Mismatches 48; Indels 20; Gaps 3;

QY 406 SPKGRFVMLPSTHTIPFYNPLHPRFPSPRLPPLPGIIGGEYDQRTPLPVYGDPISSLI 465
Db 88 SPENPFLFPQ-----PRPPRRPRPRRPSRLPP-----PLVSPPPPLH 128
QY 466 PPGGETPSPFPPLRPFRDVGPLGPNILPGRGPN-DRFPFRPSRGP 514
Db 129 PRPSPCPPPLPSPPLVSPPPPPPPSPPLVSPPPPPPPPPPPPPPPPPPP 178

RESULT 12
J80291
FB19 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: J80291
R:Totaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zelante
Biochem. Biophys. Res. Commun. 250, 555-557, 1998
A:Title: Cloning of a new gene (FB19) within HLA class I region.
A:Reference number: J80291; MUID:99003493; PMID:9784381
A:Accession: J80291
A:Molecule type: mRNA
A:Residues: 1-940 <TOT>
A:Cross-references: UNIPROT:O00405; GB:Y13247; NID:g2117158; PIDN:CAA73697.1; PID:g21171
C:Genetics:
A:Gene: FB19
A:Map position: 6p21.3

Query Match 4.0%; Score 111.5; DB 2; Length 940;
Best Local Similarity 36.8%; Pred. No. 6.9;
Matches 39; Conservative 6; Mismatches 40; Indels 21; Gaps 6;
```

QY 424 FYPNPLHPRPPSSRLPGIIGGYDQRTPLPVYVGDPISSLIIPGGETPSQPPPLRPRFD 483
Db 643 PPPGGGMPGPHGG-PGGVGPRLGPPPPPRGGDPFWD---GPGD-PMRGGPNRG--- 694
QY 484 PVGULPGNPLPGRGG-----PNDRPPFRPSR-----GRPTDGR 518
Db 695 --GPGGPGVHRGGRGGNEPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 738
RESULT 13
T49187
hypothetical protein MAA21.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49187
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25018
A:Accession: T49187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1097 <R1E>
A:Cross-references: UNIPROT:Q9LY69; EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.90
A:Experimental source: cultivar Columbia; BAC clone MAA21
C:Genetics:
A:Gene: ATSP:MAA21.90
A:Map position: 3
A:introns: 106/2; 124/3; 165/3; 198/1; 210/2; 245/3; 265/1; 297/3; 337/3; 352/1; 394/1;
Query Match 4.0%; Score 111; DB 2; Length 1097;
Best Local Similarity 20.2%; Pred. No. 9.4;
Matches 111; Conservative 75; Mismatches 218; Indels 146; Gaps 26;
QY 37 TWGY-----SNTFTITLVKDPDGTDEETLASYGVSGDLICLIQDD-IPAPN 86
Db 435 TWGLLKIMFEEBGTSTKLISHLGFTLVAEKDQAVDG---LSSDLNGIRLEDTAADALD 491
QY 87 IPSSTDSHSSIQNEQ-----PSLATSSNOTSMDEOPSD---SFGQAAQSGVWNDD 138
Db 492 LDDSEAAAFAMNGEDFNFPAPKDPDTPVSTSAKDFMPSTDFTSKGETQEMOESEE 551
QY 139 MLGP-----SQNFAESIQDN---AHMAEGTGFPYS--EPMCLSES 174
Db 552 SSDPVFDNAIQALIVGDYKEAVDQCITANKWADALVIAHV-GTALWESTREKYLKTS 610
QY 175 -----VSGVPHSLETLYQSADCSNDALIVLHLLMLESYIPQGTAKALSMPEKW 228
Db 611 APYMKVSAWNVNDRSLIYTRSHKFWKETALLC-----TFAQGEQW 653
QY 229 KLSGVYKLYMHPLCEGSSATITCVPLGN-LIVVNATLKINNEIRSVKRLQLLPESFICK 287
Db 654 T-----TLCDALASKL--MAAGNTLAALVCYCAGNVDRIVE-----INRSLSAN 696
QY 288 EKLGENVANIYKDLQKLSRLFKDQIVYPLLA----FTRQALMLPDVFGVLVLP----LELK 340
Db 697 ERDGRSYAELLQDIMEKT-----LVLAATGNKKFSASLCKLPESYAEILLASQGLTTA 750
QY 341 LAIFRLLD-----VRSVLSSAVCRDLFTAS-----NDPLLRFVLYR 378
Db 751 MKYLVLDSSGLSPELSILDRISLSABFETNTTASGNTPOQSTPMYQNQETQAQFNVLA 810
QY 379 DFRDNTVRVQDQDWKELYRKRIHQKESPKGRFVMLLPSSSTHTIP---FYNPPLHPRFP 435
Db 811 NPYDNOYQOPTYDSYVQVSH-----PFMQPTWFMFHQAQPAQPSFTAPT--SNAQP 864
QY 436 SSR-----LPPGIIGGYDQRTPLPVYVGDPISSLIIPGGETPSQPPPLRPRFDVGPL- 488
Db 865 SMRTTFVSTPALKNADQYQOPTMS-----SHSFTGTGSNNAYVPVPGPGQYAFSGFSQ 918
QY 489 --PGNPLP 496
Db 919 LQYENPKMP 928

RESULT 14
S57447
HPRII-7 protein - human
N:Alternate names: HPRII-4 protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S57447; S57489
R:Fleischhauer, K.L.
submitted to the EMBL Data Library, June 1992
A:Reference number: S57447
A:Accession: S57447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <FLB>
A:Cross-references: UNIPROT:Q16630; EMBL:X67336; NID:9871300; PIDN:CAA47751.1; PID:98713
A:Accession: S57489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-551 <FL2>
A:Cross-references: EMBL:X67337; NID:9871298; PIDN:CAA47752.1; PID:9871299
C:Genetics:
A:introns: 231/3
A:Superfamily: ribonucleoprotein repeat homology
F:82-151/Domain: ribonucleoprotein repeat homology <RRM4>
Query Match 4.0%; Score 110.5; DB 2; Length 551;
Best Local Similarity 31.1%; Pred. No. 3.7;
Matches 41; Conservative 9; Mismatches 39; Indels 43; Gaps 8;
QY 408 KGRFVMLLPSTHTTPFYPNPL-----HPRPPSSRLPGIIGGYDQRTPLPVYVGDPISS 463
Db 204 RGRPGAVGGRD-----PPGAGPGGPPPPPPAGGTPP-----RPLGPPGPPGPP 250
QY 464 LIPGGET---PSQPPPLR-----PRFDPVGLP-PGNPLPGRGGFN 502
Db 251 GPPEPGQVLPPLAGPNRGRDPPPPVLPFGQPPFQP---PLGLPPGPPPPVPGYGGPP 307
QY 503 DRFPFRPSRGRP 514
Db 308 G-PPPPQQGPP 317
RESULT 15
A54964
spliceosome-associated protein SAP-49 - human
C:Species: Homo sapiens (man)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A54964
R:Champion-Arnaud, P.; Reed, R.
Genes Dev. 8, 1974-1983, 1994
A:Title: The prespliceosome components SAP 49 and SAP 145 interact in a complex implicat
A:Reference number: A54964; MUID:95047348; PMID:7958871
A:Accession: A54964
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-424 <CHA>
A:Cross-references: UNIPROT:Q15427; GB:LJ5013; NID:9556216; PIDN:AAAG0300.1; PID:g556217
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
F:14-81/Domain: ribonucleoprotein repeat homology <RRM4>
F:101-169/Domain: ribonucleoprotein repeat homology <RRM2>
Query Match 4.0%; Score 110; DB 2; Length 424;
Best Local Similarity 32.0%; Pred. No. 2.8;
Matches 39; Conservative 9; Mismatches 32; Indels 42; Gaps 9;
QY 430 HPRPPSSRLP-PGI-----IG-----GEYDQRTPLPVYVGDPISSLIIPGPG 469
Db 292 HPHPFPFGMPHFGMSQMLAHGHGHPAGPPGSGGQPPPPPPG-----MPHPG 345
QY 470 ETPSQFFPLRPRF-DFV---GFLP-----GNPLPGRG--GPNDRFFRPSRG-----R 513

Db 346 PPFMCMPPRGPFEGSPMGHGFPMPPHGMGPPPLMPPHCGYTGPPRPPPYGYORGLDPPR 405

Qy 514 PT 515

Db 406 PT 407

Search completed: July 19, 2005, 20:20:14
Job time : 22 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:09:48 ; Search time 171 Seconds
(without alignments)
1563.189 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754

Sequence: 1 MRLRVLLKRTWPLEVPETE.....DRFPFRPSGRPTDGLSLFM 522

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2748	99.8	522	1	FBX7_HUMAN	Q9Y211 homo sapien
2	1984	72.0	522	2	Q6RFS3	Q6RFS3 rattus norv
3	1977.5	71.8	523	2	Q8K0A5	Q8K0A5 mus musculus
4	1295	47.0	361	2	Q6Y0L7	Q6Y0L7 gallus gall
5	1125	40.8	478	2	Q6DE59	Q6DE59 xenopus lae
6	240.5	8.7	475	2	Q9ZUB8	Q9ZUB8 arabidopsis
7	205	7.4	776	2	Q8GZV6	Q8GZV6 oryza sativ
8	187.5	6.8	350	2	Q9ZUB9	Q9ZUB9 arabidopsis
9	147	5.3	270	1	PSF1_DROME	Q9V637 drosophila
10	145.5	5.3	434	2	Q9Y593	Q9Y593 homo sapien
11	144	5.2	403	2	Q6PKH7	Q6PKH7 homo sapien
12	144	5.2	437	2	Q9NT57	Q9NT57 homo sapien
13	144	5.2	447	1	FBX7_HUMAN	Q9UK97 homo sapien
14	138.5	5.0	356	2	Q7ZTY2	Q7ZTY2 brachydanio
15	135	4.9	436	2	Q8VDY6	Q8VDY6 mus musculus
16	135	4.9	437	2	Q8BK06	Q8BK06 mus musculus
17	134.5	4.9	1183	2	Q7TSH6	Q7TSH6 mus musculus
18	134.5	4.9	1209	2	Q6PFF0	Q6PFF0 mus musculus
19	134	4.9	3148	2	Q8H6Q8	Q8H6Q8 poncirus tr
20	129.5	4.7	1200	2	Q69ZP8	Q69ZP8 mus musculus
21	129	4.7	745	2	Q6Z1Z5	Q6Z1Z5 oryza sativ
22	128.5	4.7	850	2	Q17055	Q17055 caenorhabdi
23	126.5	4.6	431	2	Q7SV92	Q7SV92 xenopus lae
24	126	4.6	355	1	FX32_HUMAN	Q969P5 homo sapien
25	123	4.5	271	1	PSF1_HUMAN	Q92530 homo sapien
26	123	4.5	936	2	Q8QRV7	Q8QRV7 pongine her
27	122	4.4	953	2	Q6MB50	Q6MB50 parachlamyd
28	120.5	4.4	888	2	Q6P9Q5	Q6P9Q5 mus musculus
29	120.5	4.4	911	2	Q8CIE2	Q8CIE2 mus musculus
30	120.5	4.4	925	2	Q8NPF4	Q8NPF4 homo sapien
31	120	4.4	271	2	Q8BHL8	Q8BHL8 m mus muscu

32	120	4.4	684	1	CDC4_CANAL	P53699 candida alb
33	120	4.4	1255	2	Q9R2J6	Q9R2J6 plasmod col
34	119	4.3	271	2	Q8C0G9	Q8C0G9 mus musculus
35	119	4.3	287	2	Q95UG5	Q95UG5 babesia bov
36	119	4.3	844	2	Q9R2J5	Q9R2J5 plasmod col
37	118	4.3	442	2	Q9VG61	Q9VG61 drosophila
38	118	4.3	564	2	O53539	O53539 mycobacteri
39	118	4.3	564	2	Q7TWD7	Q7TWD7 mycobacteri
40	117.5	4.3	503	1	WAIP_HUMAN	Q43516 homo sapien
41	117.5	4.3	1179	2	Q9NQW1	Q9NQW1 homo sapien
42	117.5	4.3	1213	1	FMN_CHICK	Q05858 gallus gall
43	117	4.2	2167	1	SHK1_RAT	Q9W48 rattus norv
44	116.5	4.2	210	2	Q8TC93	Q8TC93 homo sapien
45	116.5	4.2	592	1	ODP2_DICDI	P36413 d dihydroli

ALIGNMENTS

RESULT 1
ID FBX7_HUMAN STANDARD; PRT; 522 AA.
AC Q9Y3I1; Q9EHM6; Q9UF21; Q9UKT2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE F-box only protein 7.
GN Name=FBX07; Synonym=FBX7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 41-522 FROM N.A.
RX MEDLINE=200303060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiar D.S., Guardavaccaro D., Parks W., Vidal M.,
RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20399565; PubMed=10945468; DOI=10.1006/geno.2000.6211;
RA Ilyin G.P., Riiland M., Pigeon C., Gugen-Guilouzo C.;
RT "cDNA cloning and expression analysis of new members of the mammalian
RL F-box protein family.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,

RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.I.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wansley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Haller L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuwa H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT Nature 402:489-495(1999).
RL [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC -!- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
CC (By similarity).
CC -!- SIMILARITY: Contains 1 F-box domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF129537; AAF04471.1; -;
CC EMBL; AF232225; AAF67155.1; -;
CC EMBL; AL050254; CAB43356.1; -;
CC EMBL; J71183; CAB63143.1; -;
CC EMBL; BC008361; AAH08361.1; -;
CC Genew; HGNC:13586; PBX07.
CC MIM; 605648; -;
CC GO; GO:0000151; Cubiquitin ligase complex; TAS.
CC GO; GO:0004842; Fubiquitin-protein ligase activity; TAS.
CC GO; GO:0006511; Fubiquitin-dependent protein catabolism; TAS.
CC InterPro; IPR001810; F-box.
CC InterPro; IPR008945; Skp1_Skp2.
CC Pfam; PF00646; F-box; 1.
CC PROSITE; PS0181; FBOX; 1.
KW Ub1 conjugation pathway.
DOMAIN 329 375 F-box.

FT CONFLICT 41 41 S -> M (in Ref. 1).
FT CONFLICT 79 79 Q -> H (in Ref. 1).
FT CONFLICT 84 84 A -> P (in Ref. 1).
FT CONFLICT 115 115 M -> I (in Ref. 1 and 4).
FT CONFLICT 169 169 M -> L (in Ref. 1).
FT CONFLICT 224 224 M -> L (in Ref. 1).
FT CONFLICT 241 241 P -> H (in Ref. 1).
FT CONFLICT 328 328 D -> N (in Ref. 1).
FT CONFLICT 413 413 M -> L (in Ref. 1).
FT CONFLICT 475 475 F -> L (in Ref. 1).
SQ SEQUENCE 522 AA; 58502 MW; CAE5E70A0747287A CRC64;
Query Match 99.8%; Score 2748; DB 1; Length 522;
Best Local Similarity 99.8%; Pred No. 3 9e-174;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRLRVLLKRTWPLEVPEPETGLHRLSHRLSLCTWGYSSNTRFTITLNYKDLTGDE 60
DB 1 MRLRVLLKRTWPLEVPEPETGLHRLSHRLSLCTWGYSSNTRFTITLNYKDLTGDE 60
QY 61 ETLASYGIVSGDLICLLILODDIPAPNIPSSSTDSEHSSLONNPEOPSLSATSSNOTSWODEP 120
DB 61 ETLASYGIVSGDLICLLILODDIPAPNIPSSSTDSEHSSLONNPEOPSLSATSSNOTSWODEP 120
QY 121 SDSFOGQAQSGVWDDSMGLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVGQVP 180
DB 121 SDSFOGQAQSGVWDDSMGLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVGQVP 180
QY 181 HSLETLYSADCSANDALIIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLYQVNH 240
DB 181 HSLETLYSADCSANDALIIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLYQVNH 240
QY 241 PLCEGSSATLCVPLGNLIVVNATKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
DB 241 PLCEGSSATLCVPLGNLIVVNATKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
QY 301 LQKLSRLFKDQLVYPLLAFTQALMLPDVFGIIVLPLELKLRIFFLLDVRSLSAVCR 360
DB 301 LQKLSRLFKDQLVYPLLAFTQALMLPDVFGIIVLPLELKLRIFFLLDVRSLSAVCR 360
QY 361 DLFTASNDPLWRFLYLDRDNDNTVRVQDTWKELYRKHQRKESPKGRFVMLLPSSSTH 420
DB 361 DLFTASNDPLWRFLYLDRDNDNTVRVQDTWKELYRKHQRKESPKGRFVMLLPSSSTH 420
QY 421 TIPFPNPLHRRPPSSRLPGIIGEDYDQRTPLVYGDPTLSLLIPGGETSQPPPLRP 480
DB 421 TIPFPNPLHRRPPSSRLPGIIGEDYDQRTPLVYGDPTLSLLIPGGETSQPPPLRP 480
QY 481 RFDVPVGPPLPGNPILPGRGGPNDRPFRPSRGRPTDGRLSFM 522
DB 481 RFDVPVGPPLPGNPILPGRGGPNDRPFRPSRGRPTDGRLSFM 522
RESULT 2
Q68F53 PRELIMINARY; PRT; 522 AA.
AC Q68F53
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 DR Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC079382; AAH79382.1; -;
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR PROSITE: PS50181; FBOX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 522 AA; 57560 MW; 1A1E5C131425CD7B CRC64;

Query Match 72.0%; Score 1984; DB 2; Length 522;
 Best Local Similarity 72.3%; Pred. No. 2.1e-123;
 Matches 378; Conservative 57; Mismatches 86; Indels 2; Gaps 2;

QY 1 MRLVRLKRTWPPEPTLGLHRLSLCTWGYSNTRFTITLNYKDLPTGDE 60
 DB 1 MKLRLVLRKRTQPLEVPSEPTLGLRAHLIQDLPLTLGFSSTDFRFAITLNKDALTGDE 60

QY 61 ETLASGIVSGDLICLILODDIPAPNIPSTSEHSSLONNQPSLATSSNQTSMODEQP 120
 DB 61 ETLASGIVSGDLICLVLEDDMPAPNLPSTSEHSSLONNQPSLATSSNQTSMODEQP 120

QY 121 SDSFOQAQSGVNDSDMLGSPONFEASIDONAHMAGTGFYPSEPMLCSEVGGVP 180
 DB 121 SDSHGQVQYDAWTDSDMEGSHSAEVSIDAMSEVSGFHPLEPMLCSETEGQVP 180

QY 181 HSLETLYQSADCSNDALIVLHLLMESGYIPQGTAKALSMPEKWLKSGYKLYQYMH 240
 DB 181 HSLEALYQSAGCSNVDALIVLHLLMESGYIPQGTAKALSMPEKWLKSGYKLYQYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVNATKINNEIRSVKRLQLLPESFCKEKLGENVANIYK 300
 DB 241 PLCEGSSAVLTTCVPLGKLIMINATIKVNGGIKNVKSQVLKPGAYVRRASPGESAARYK 300

QY 301 LOKLSRLFKDQVLPYLLAFTFQALNLPDVGVLVPLLEKLRIFRLLDVRSVLISAVCR 360
 DB 301 LKLSRLFKDQVLPYLLAFTFQALNLPDVGVLVPLLEKLRIFRLLDVRSVLISAVCH 360

QY 361 DLFTASNDPLLWRFLYLRDFRNTVRVQDTDWKELYRKHHIQRKESPKGRFVMLLPSSHT 420
 DB 361 DLLIASNDPLLWRFLYLRDFRNTVRVQDTDWKELYRKHHIQRKESPKGRFVMLLP-SVH 419

QY 421 TTPFPNPLHPRFP-PSSRLPGIITGGEYDQRTPLPYVGDPISLIPGGETPSPFPPIR 479
 DB 420 PIPFCPIPYRPLPTLLPPIGGEYDERPILPSVGDPTVTSIPRPGEPSPQPRVR 479

QY 480 PRFDPVGPLPGNPILPGRGGNDPRPFRPGRPTDGRLSFM 522
 DB 480 PRFDPVGPLPGNSLLPGRASNNRPPFRPGRGRSADNRLPYL 522

RESULT 3
 Q8K0A5 PRELIMINARY; PRT; 523 AA.
 ID Q8K0A5
 AC Q8K0A5;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE F-box only protein 7.
 GN Name=Fbxo7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Klausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032153; AAH32153.1; -;
 DR MGI:1917004; Fbxo7.
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR PROSITE: PS50181; FBOX; 1.
 DR SEQUENCE 523 AA; 57634 MW; ABFD250070C1FEB5 CRC64;

Query Match 71.8%; Score 1977.5; DB 2; Length 523;
 Best Local Similarity 72.5%; Pred. No. 5.6e-123;
 Matches 380; Conservative 56; Mismatches 85; Indels 3; Gaps 3;

QY 1 MRLVRLKRTWPPEPTLGLHRLSLCTWGYSNTRFTITLNYKDLPTGDE 60
 DB 1 MKLRLVLRKRTQPLEVPSEPTLGLRAHLISQVLLPTLGLFSSDTRFAITLNKDALTGDE 60

QY 61 ETLASGIVSGDLICLILODDIPAPNIPSTSEHSSLONNQPSLATSSNQTSMODEQP 120
 DB 61 ETLASGIVSGDLICLVLEDDMPAPNLPSTSEHSSLONNQPSLATSSNQTSMODEQP 120

QY 121 SDSFOQAQSGVNDSDMLGSPONFEASIDONAHMAGTGFYPSEPMLCSEVGGVP 180
 DB 121 TDSGQATPFDWTDSDMEGSHSAEVSIDAMSEVSGFHPLEPMLCSETEGQVP 180

QY 181 HSLETLYQSADCSNDALIVLHLLMESGYIPQGTAKALSMPEKWLKSGYKLYQYMH 240
 DB 181 HSLETLYQSAGCSNVDALIVLHLLMESGYIPQGTAKALSMPEKWLKSGYKLYQYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVNATKINNEIRSVKRLQLLPESFCKEKLGENVANIYK 299
 DB 241 PLCEGSSAVLTTCVPLGNLIIINATIKVNGGIKNVKSQVLKPGAYVRRASPGESAARYK 300

QY 300 LOKLSRLFKDQVLPYLLAFTFQALNLPDVGVLVPLLEKLRIFRLLDVRSVLISAVC 359
 DB 301 DLKLSRLFKDQVLPYLLAFTFQALNLPDVGVLVPLLEKLRIFRLLDVRSVLISAVC 360

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QY 360 RDLFTASNDPLLRFLYLDRDNTVRVQDITDWKELYRKHRIQKESPKGRFVWMLLPST 419
Db 361 HDLLIASNDPLLRCLYLDRDFDGTGVRGDTIDWKELYRKHRIQKESPKGRHMFPSA- 419
QY 420 HTIPYPNLHPRPF-PSRLPBGIIIGGEYDORPILPVGDPISSILIPGPGTTPSQFPL 478
Db 420 HPFPCPIPVYRAYLPTSLPBGIIIGGEYDERRILPSVGDPIVTSILIPRPGELPQFRPL 479
QY 479 RRPDPVGLPGLPGLPGRGGPNDRFPFRSGRGTDRGLSFM 522
Db 480 RRPDPVGLPGLPGLPGLPGLPGLPGLPGLPGLPGLPGLPGLPGLPGLPGLPGLPGL 523

RESULT 4
Q6YOL7 PRELIMINARY; PRT; 361 AA.
AC Q6YOL7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE F-box only protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_
RP SEQUENCE FROM N.A.
RA Emaru M.G., Kim H.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194289; AAP83452.1; -.
DR EMBL; AY194288; AAP83452.1; JOINED.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS0181; FBOX; 1.
FT NON TER 1
SQ SEQUENCE 361 AA; 40110 MW; 51C54C0292833884 CRC64;

Query Match 47.0%; Score 1295; DB 2; Length 361;
Best Local Similarity 65.6%; Pred. No. 6.9e-78;
Matches 246; Conservative 47; Mismatches 62; Indels 20; Gaps 4;

QY 153 DNAHAEGTGYFSPMLCSVEGVPHSLTLYQSADCSNDALIVLHLLMLESY 212
Db 2 EDVDLEEGTGYFSPMLCSVEGVPHSLTLYQSADCSNDALIVLHLLMLESY 61

QY 213 IPQGTAKALSMPEKWKLVGVYKLYQVHPLCGSSATLTCVPLGNLIVVNATLKINNEIR 272
Db 62 VPQGTAKAVSMPEKWRGNGVYKLYQVHPLCGSSATLTCVPLGNLIVVNATLKINNEIR 121

QY 273 SVKRIQLLPESPTCKELGENTVANIYKDLKSLRFLKDLVYPLAFTQALNLPDVVGL 332
Db 122 GVKRIQLLPASVFCQE-PEKVAGVYKDLKSLRFLKDLVYPLAFTQALNLPDVVGL 180

QY 333 VVLPLELKLIRIFRLDVRVLSISAVCRDLFTASNDPLLRFLYLDRDNTVRVQDITDW 392
Db 181 VVLPLELKLIRIFRLDVRVLSISAVCRDLFTASNDPLLRFLYLDRDNTVRVQDITDW 392

QY 393 KELYRKHRIQKESPKGRFVWMLLPSTHTIPFPNPLHPRFPFSSRLP-----PGIIGE 447
Db 228 SELYKKKLQKKEALRRH-MFLPTTPHPIPHNPFPYSPFPNPPFPNPIYPPMWIGE 286

QY 448 YQORPTLPVGDPISSILIPGPGTTPSQFPLPDRPDVGLPGLPGLPGLPGLPGLPGLPGL 507
Db 287 YGERPTLLYIGDPIINSILIPGPGTTPSQFPLPDRPDVGLPGLPGLPGLPGLPGLPGLPGL 346

QY 508 RPSRGPTDGRLSFM 522
Db 347 RPSRGPTDVRRAFI 361

RESULT 5
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Q6DE59 PRELIMINARY; PRT; 478 AA.
ID Q6DE59;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE Fbox7-prov protein.
GN Name=fbox7-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]_
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]_
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077283; AAH77283.1; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001226; Flavodoxin.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS0181; FBOX; 1.
DR PROSITE; PS0201; FLAVODOXIN; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53251 MW; 8C12F01E32C1873F CRC64;

Query Match 40.8%; Score 1125; DB 2; Length 478;
Best Local Similarity 47.5%; Pred. No. 2e-66;
Matches 251; Conservative 74; Mismatches 147; Indels 56; Gaps 14;

QY 1 MBLRVLRLKRPWLEVPETETLGLRSHLRSLILCTWGYSSNTFTITLVNKKDPLTGD 60
Db 1 MBLRVLRLKRPWLEVPETETLGLRSHLRSLILCTWGYSSNTFTITLVNKKDPLTGD 60

QY 61 ETLSAGYIVSGDLICLILOD--DIPAPNIPSTDSHSSLNQNEQPSLATSSNQTSMQDE 118
Db 61 TTLESAGIISGDLIVLLPDPQLAPPAPERD-PRCELEDPTQP-----CSTANK 111

QY 119 QPSDSFGQAAQSGVWVNDSDMLGSPNFSESIONAHMAEGTGYPG-EPMLCSSEV 177
Db 119 QPSDSFGQAAQSGVWVNDSDMLGSPNFSESIONAHMAEGTGYPG-EPMLCSSEV 177
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DR InterPro; IPR001810; F-box.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR002029; Pept_S8_S53.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 776 AA; 83902 MW; F05B3429D2B924BD CRC64;

Query Match 7.4%; Score 205; DB 2; Length 776;
Best Local Similarity 22.0%; Pred. No. 4.6e-05;
Matches 115; Conservative 90; Mismatches 197; Indels 120; Gaps 25;

QY 1 MELRVLLKR-----TWPLEVPETEPTLGLRSLRLSLCTGWYSSNTRFTITLN 51
Db 1 MKLRURSDQRGGAGAAETHRVQLPDT--ATLSDVKAFIATKLSAAQPVPAES-VRLTLN 58
QY 52 YKDP-LTGD-BETLASYGIVSGDLICLIQDDIPAPNIPSSDSEHSSLNQNN---EQPSL 106
Db 59 RSEELLTPDPSATLPALGLASGDLLYFTL-SPLSPSPPPQPOQAQPLPRNPNPDVPSI 117
QY 107 ATSSNOTSQDQPSDSFGQAAQSG----VWDDSMGLGPSQNFBAESIQDNAHMAEGTG 162
Db 118 AGAADPTKSPVBSGSSSSMPQALCTNPGLPVASDPHHPPP-----DVWMAEAPA 166
QY 163 FYPSPMLCSVEQGVPHSLTQVSAD----CSDANDALIVLIHLLMLESYIPQGTTE 218
Db 167 VTYSK-----SSLVGDTKREMN-V-GGADGTVC-----RLVVAAHALLDAGFIYANPV 216
QY 219 AKALSMPEKWKLSGVY---KLOYMHP-----LCEGSSATLTCVPLGNLIVVNATLKI 267
Db 217 GSCLQLPQNW-ASGSFVPVSMKYTLPELVEALPVVEEGWAVLVNLSMGFMVYVYV-G-HV 273
QY 268 NNEIRSVKRL-----QLLPESFICEKLGENVANYIKOLQKLSRLFKOOLVYPLLAFTQ 322
Db 274 PGATSGVRLCLPELAPLALYLDSDDEVSTABE---REIHELWRLVKDQEMCLMISLCQ 330
QY 323 ALNLPDVFGLVPLLELKLIRFLDLVRSVLSAVCRDLFTASNDPLFLYLRDERD 382
Db 331 LNNLSLPPCLMALPGDVKAKVLEFVFGVDLRAVQCTCKELRLDLAADDNLWKKKCEMEF-- 388
QY 383 NTVRVQDT----DWKELY---RK-----RHIQRKESPKGRFVMLL-----415
Db 389 NT---QDTGCMWCKCIYSDQRKDIVLADKYTCGNVMQKPVTPQGRWLLIIVYHSLCQY 445
QY 416 -----PSTTWTTPYPNPLHPRPPSS 437
Db 446 ITIGLSLLWYHLVDLVAQAPAAAGIHFDICIPLINPYQLPPS 487

RESULT 8
Q9ZUB9
ID PSF1_DROME PRELIMINARY; PRT; 350 AA.
AC Q9ZUB9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE F508.32 protein.
GN Name=F508.32;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RA SEQUENCE FROM N.A.

Vsotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
Li J., Kremenetskaia I., Luros J., Altafi H., Gonzalez A., Araujo R.,
Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L.,
Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
Ecker J.R., Federspiel N.A., Theologis A.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Theologis;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005990; AAC98032.1; -.
DR PIR; H86371; H86371.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 350 AA; 39953 MW; CD0BD4C6791674D6 CRC64;

Query Match 6.8%; Score 187.5; DB 2; Length 350;
Best Local Similarity 24.4%; Pred. No. 0.00022;
Matches 90; Conservative 58; Mismatches 118; Indels 103; Gaps 17;

QY 172 SESVEGQVPHSLE-----TLYOSADCSANDALIVLIHLLMLESYI 213
Db 22 NSGIEGVPMDVELAAAKSKRLSEPFLLKNVLEKSGDTSILT-ALALSVHVMLESQV 80
QY 214 --PQGTTE-----AKALSMPEKWKLSGVYKLYQMHPCLCEGSSATLTCVPLGNLIVVNATL- 265
Db 81 LLDHSGDKFSFKLLSVSLRYTLPELITRKDNTV---ESVTVRFQWIGPRLVYGTILG 137
QY 266 ---KINNEIRSVKRLQLLPESFICEKL---GENVANYIKOLQKLSRLFKOOLVYPLIA 318
Db 138 GSKRVH--MISLDSKRLPVIDLVVDITLKEKQSGSSYREVFMWRMVKDELVIPL- 194
QY 319 FTRQALNLPDVFG-----LVVLPLELKLIRFLDLVRSVLSAVCRDLFTASNDPLW 372
Db 195 -----IGLCDKAGLESPPCLMLLPTELKILLELPGVSGMACVCTEMRYLASDNDLW 249
QY 373 RFLYLDRDNTVRVQ---DTWKELY---RKR---HIQRKESPKGRFVMLLPSSTHTIP 423
Db 250 EHKCLUEGKGLWKLYTGDVWKRFASFWRKRRLDLLARRNPPIKK-----296
QY 424 FYPNPLHPRPPSSRLPPGIIGGYDQRPITLYVGDPISSLIIPGGETPSPQFPL- 478
Db 297 --SNRFFTLPPDR-----DREPPDRFG-----PSDFYREGLRDP 331
QY 479 RPRPDVPG 487
Db 332 RDRFGPRDP 340

RESULT 9
PSF1_DROME
ID PSF1_DROME STANDARD; PRT; 270 AA.
AC Q9V637;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Putative proteasome inhibitor.
GN ORFNames=CG8979;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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Db 210 CRGFYICARDPEIWLRLACKVWGRSCIKLVPTYSWREMFLEPRVRFQGVYIS 262
QY 418 ST-----HTIPFYFNPLHPPFPSSRLPPGIIIGGYDQRTPLPYVGDP 460
Db 263 KTYIIRQGEQSLDGFYRAWHQVEYY---RYIRFFPDGHV----- 298
QY 461 ISSLIPGCGETPSQPPPLRPR 481
Db 299 --MMLTTPPEQSIIVPLRLTR 317

RESULT 13
FBX9 HUMAN
ID FBX9 HUMAN STANDARD; PRT; 447 AA.
AC Q9UK97; 075986;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE F-box only protein 9.
GN Name=FBX9; Synonyms=FBX9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20030361; PubMed=10531037; DOI=10.1016/S0960-9822(00)80021-4;
RA Winston J.T., Koepf D.M., Zhu C., Elledge S.J., Harper J.W.,
RT "A family of mammalian F-box proteins.";
RL Curt. Biol. 9:1180-1182(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Cullley K.M., Dhali P., Davies J., Dunn M., Earthrow M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gillson C.J., Glithero R.J., Graham D.V., Grant M.,
RA Gribble L., Griffiths C., Griffiths M.N.D., Hall R., Hall K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.L., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RT "The DNA sequence and analysis of human chromosome 6.";
RL Nature 425:805-811(2003).
RN [3]
RP SEQUENCE OF 121-447 FROM N.A.
RX MEDLINE=20030360; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiau D.S., Guardavaccaro D., Parks W., Vidal M.,

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RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curt. Biol. 9:1177-1179(1999).
CC FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation.
CC SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
CC (By similarity).
CC SIMILARITY: Contains 1 F-box domain.
CC SIMILARITY: Contains 1 TPR repeat.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF176704; AAF03704.1; -;
CC EMBL; AL031178; CAA20122.1; -;
CC EMBL; AF174597; AAF04518.1; -;
CC Genew; HGNC:13588; FBX9.
CC GO; GO:0000151; C:ubiquitin ligase complex; NAS.
CC GO; GO:0004842; E:ubiquitin-protein ligase activity; NAS.
CC GO; GO:0016567; F:protein ubiquitination; NAS.
CC InterPro; IPR001810; F-box.
CC InterPro; IPR008945; Skp1 Skp2.
CC InterPro; IPR008941; TPR-like.
CC Pfam; PF00646; F-box; 1.
CC PROSITE; PS50181; FBOX; 1.
KW TPR repeat; Ubi conjugation pathway.
FT REPEAT 94 127
FT DOMAIN 185 236 F-box.
SQ SEQUENCE 447 AA; 52329 MW; 2A88163DAB898D69 CRC64;

Query Match 5.2%; Score 144; DB 1; Length 447;
Best Local Similarity 23.1%; Pred. No. 0.24;
Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKQVYHPLCEG-SSATLTCVPL---GNLTWVATLKINNE-----IRSV-- 274
Db 45 MFRQWMEFAPGVSSNLENRPCCARAGSLQKTSADTKGQKQKAEKARELFKAVSE 104
QY 275 -----KRLQLPE-----SFICKEKLGENVANIY---KOLQKLSRL---PK 309
Db 105 EQNGALYEAIRFYRRAMQLVPDIEFKITVTRSPDGVGVNSYIEDNDDSKMALLSYFQ 164
QY 310 DQLVYPLLAFTQALNL--PDV-----FGLVLPLEKLRIPL-----LDVRSVLISLV 358
Db 165 QQ-----LTFQESVLKLCQPELESSQIHISVLPMELVMYIFRWVWSSDLDRSLQSLV 219
QY 359 CRDLFTASNDPLLWRFYLRDFRDNTVR-VQDTPDKELYRKHIQKESPKGRFVMLLPS 417
Db 220 CRGFYICARDPEIWLRLACKVWGRSCIKLVPTYSWREMFLEPRVRFQGVYIS 272
QY 418 ST-----HTIPFYFNPLHPPFPSSRLPPGIIIGGYDQRTPLPYVGDP 460
Db 273 KTYIIRQGEQSLDGFYRAWHQVEYY---RYIRFFPDGHV----- 308
QY 461 ISSLIPGCGETPSQPPPLRPR 481
Db 309 --MMLTTPPEQSIIVPLRLTR 327

RESULT 14
Q7ZTY2
ID Q7ZTY2 PRELIMINARY; PRT; 356 AA.
AC Q7ZTY2
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Similar to F-box only protein 32.
GN ORFNames=zgc:56479;

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OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Leckman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC052112; RAHS2112.1; --
DR ZFIN; ZDB-GENE-040426-1040; zgc:56479.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 356 AA; 41897 MW; 21F8A1E90B45DC2 CRC64;

Query Match 5.0%; Score 138.5; DB 2; Length 356;
Best Local Similarity 27.1%; Pred. No. 0.41;
Matches 62; Conservative 31; Mismatches 75; Indels 61; Gaps 11;

QY 230 LSGVYKLYMHPLCEGSSATLTCVPLGNLI--VNNATLKINNEIRSVKRLQLLPESFICK 287
Db 138 LSGVAQKNY-----NILERVQKVLDDQNVPRIKELLQTLVASLCS 180

QY 288 --EKLGENV-----ANIYKDLQKLSRLFKDQLVYPLLAFTQAALNLPVFG-- 331
Db 181 LVQDNGKSVLGNINIWHRMENILQWQQLDNI-----QINRPKNTGMT 225

QY 332 LVVLPLEKLRF--RLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDFRDNVTR-- 386
Db 226 LLELPVSLQNLIMQRLSDGRDLVSLGQVCPDLMLTEBRLMKKLCQHTDRQIRKRLM 285

QY 387 VQD---TDWKLYKRKHQRKSPKGRFVMLPSSTHT-IPFPNPLHP 431
Db 286 VSDKGQLEWKMYFK--LCRCYPKHEQYSDTLQFCTCHILFWKDTDHP 332

RESULT 15
Q8VDY6 PRELIMINARY; PRT; 436 AA.
AC Q8VDY6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fbxo9 protein.

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GN Name=Fbxo9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Leckman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC020074; AAH20074.1; --
DR MGD; MGI:1918788; Fbxo9.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 436 AA; 50672 MW; 3479C6C144A26805 CRC64;

Query Match 4.9%; Score 135; DB 2; Length 436;
Best Local Similarity 22.7%; Pred. No. 0.93;
Matches 57; Conservative 41; Mismatches 67; Indels 86; Gaps 11;

QY 275 KRLQLLP-----SFICKEKLGENVANIY----KDLQKLSRLFKDQLVYPLLAFTQAALNL 326
Db 108 RAMQLVPDIEFKITYRSPDGDGSGVYIENEDASKVA-----DLSYFQOQLTL 158

QY 327 -----PDV----FGLVVLPLELKLRIPL-----LDVRSVLSLSAVCRDLFTASND 368
Db 159 QESVLKLCQPELETSTQTHISVLPMVEVLWYIFRWVVSDDLRLSLQLSILVCRGFYICARD 218

QY 369 PLLWRFLYLRDFRDNVTR-VQDTPWKLYKRKHQRKSPKGRFVMLPSST----- 419
Db 219 FEIWRACLKVGKRSCKMLVPYASWREMFLE-----PRVDFGVVISKTYIRQGEQ 271

QY 420 -----HTIPFPNPLHPPPSSRLPGIIGGEYDQRPPLPYVGDPISLIPGGE 470
Db 272 SLDGFYRAHWQVEYY---RYWRFPDGHV-----MLTTPEE 305

QY 471 TPSQFPPLRPR 481
Db 306 PPSIVPRLRTR 316

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Search completed: July 19, 2005, 20:19:50
Job time : 174 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:06:57 ; Search time 166 Seconds
(without alignments)
1216.198 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVLLKRTWPLEVPETE.....DRPPFRPRGRPTDGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A. Geneseq 16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	522	ADA57283	Human sec
2	2748	99.8	522	ADA41163	Human sec
3	2748	99.8	522	ABR47958	Human sec
4	2748	99.8	522	ADC74366	Human sec
5	2744	99.6	522	AAB35161	Human Skp
6	2744	99.6	522	ABM82342	Tumour-as
7	2510	91.1	591	AAW68521	Human RIP
8	2489	90.4	482	AAH83047	F-box pro
9	2489	90.4	482	AAO22452	Human F-b
10	2448	88.9	607	AAU32109	Novel hum
11	2404	87.3	462	ABB90109	Human pol
12	2404	87.3	462	ADA57586	Human sec
13	2404	87.3	462	ADA41482	Human sec
14	2404	87.3	462	ABR48139	Human sec
15	2404	87.3	462	ADC74596	Human sec
16	2270	82.4	443	AAAB35160	Human Skp
17	2086	75.8	549	ABG18510	Novel hum
18	1527	55.4	317	ABB90108	Human pol
19	1328	45.0	231	ADJ68946	Human hea
20	1086	39.4	221	ADA54155	Human pro
21	714	25.9	174	ADA57587	Human sec
22	714	25.9	174	ADA41483	Human sec
23	714	25.9	174	ABR48140	Human sec
24	714	25.9	174	ADC74597	Human sec
25	714	25.9	175	AAY41397	Human sec

ALIGNMENTS

RESULT 1
ADA57283
ID ADA57283 standard; protein; 522 AA.

AC ADA57283;

DT 20-NOV-2003 (first entry)

DE Human secreted protein #566.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

OS WO2002102994-A2.

PN 27-DEC-2002.

PD 19-MAR-2002; 2002WO-US008278.

PF 21-MAR-2001; 2001US-0277340P.

PR 13-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

XX N-PSDB; ADA56387.

XX New human secreted polypeptides and polynucleotides, useful for

XX diagnosing, treating or preventing e.g. immune disorders, inflammatory

XX conditions, respiratory disorders, cancers, CNS disorders, or

XX neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1473; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for

XX diagnosing, treating or preventing e.g. immune disorders, inflammatory

conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. Parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.6e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLLKRTWPTEPTPLGHLRSHLRSLUSLLCTWGYSSNTRFTTLNPKDPLTGD 60
DB 1 MRLRVLLKRTWPTEPTPLGHLRSHLRSLUSLLCTWGYSSNTRFTTLNPKDPLTGD 60
QY 61 ETLASGVIVSGDLICLLIQDDIPAPNIPSSDTSEHSSIQNNEOPSLSATSSNQTSMQDSQP 120
DB 61 ETLASGVIVSGDLICLLIQDDIPAPNIPSSDTSEHSSIQNNEOPSLSATSSNQTSMQDSQP 120
QY 121 SDSFQQAQSGVWDDNSMLGFSQNFESIQDNNAHMAEGTGFYSPMLCSVESVEGQVP 180
DB 121 SDSFQQAQSGVWDDNSMLGFSQNFESIQDNNAHMAEGTGFYSPMLCSVESVEGQVP 180
QY 181 HSLETLYSADCSNDALIVLIHLLMLESVYIPQGTAKALSMPEKWLKSGVYKLYMH 240
DB 181 HSLETLYSADCSNDALIVLIHLLMLESVYIPQGTAKALSMPEKWLKSGVYKLYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
QY 301 LQKLSRLFKDQVYVYLLAFTQALNLPDVGVLVPLLELKLIRFLDLVRSVLSLAVCR 360
DB 301 LQKLSRLFKDQVYVYLLAFTQALNLPDVGVLVPLLELKLIRFLDLVRSVLSLAVCR 360
QY 361 DLFTASNDPLLRFLYLRDFRNTVRVQDTWKELYKRXHQRKESPKGRFVWMLPSSHT 420
DB 361 DLFTASNDPLLRFLYLRDFRNTVRVQDTWKELYKRXHQRKESPKGRFVWMLPSSHT 420
QY 421 TTPFPNPLHPPFPSSRLPGCIIGGEYDQRTPLPYVGDPITSLIPGPGTSPQFPPLRP 480
DB 421 TTPFPNPLHPPFPSSRLPGCIIGGEYDQRTPLPYVGDPITSLIPGPGTSPQFPPLRP 480
QY 481 RFDVPGVPLPGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
DB 481 RFDVPGVPLPGPNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522

RESULT 2
, ADA41163

ID ADA41163 standard; protein; 522 AA.
XX
AC ADA41163;
XX
DT 20-NOV-2003 (first entry)
XX Human secreted protein.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnery; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1545; 3205pp; English.
XX
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.6e-239;

	Matches	521;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;			
Qy	1	MRLRVLLKRTWP	LEVPETPTLGH	RLSHLRLSL	LLCTWGYSSN	TRFTITLNYK	DP	LTGDE	60				
Db	1	MRLRVLLKRTWP	LEVPETPTLGH	RLSHLRLSL	LLCTWGYSSN	TRFTITLNYK	DP	LTGDE	60				
Qy	61	ETLASYGIVSGD	LICLILODDI	PAPNIPSS	TDSHSSLLQ	NEQPSLAT	SSNQTSMQ	DEQP	120				
Db	61	ETLASYGIVSGD	LICLILODDI	PAPNIPSS	TDSHSSLLQ	NEQPSLAT	SSNQTSMQ	DEQP	120				
Qy	121	SDSFGQAAQSG	VWNNDDSM	LGPSQNF	AEISIQDNA	HMAEGTGF	YFSEPM	LCSESV	EGQVP	180			
Db	121	SDSFGQAAQSG	VWNNDDSM	LGPSQNF	AEISIQDNA	HMAEGTGF	YFSEPM	LCSESV	EGQVP	180			
Qy	181	HSLETLYQSA	DCSDAND	ALIVLHLL	MLESYI	PGTEAKAL	SMEKWKLS	GVYKLY	QYMH	240			
Db	181	HSLETLYQSA	DCSDAND	ALIVLHLL	MLESYI	PGTEAKAL	SMEKWKLS	GVYKLY	QYMH	240			
Qy	241	PLCEGSSAT	LTCTVPL	GNLIVV	NATLKIN	NEIRSV	KRLQLP	ESFICKE	KLGENV	ANIYKD	300		
Db	241	PLCEGSSAT	LTCTVPL	GNLIVV	NATLKIN	NEIRSV	KRLQLP	ESFICKE	KLGENV	ANIYKD	300		
Qy	301	LQKLSRLFK	DQLVYPL	LAFTQAL	NLPDV	FGVLVPL	ELKLRIF	RLLDV	RSVLS	SAVCR	360		
Db	301	LQKLSRLFK	DQLVYPL	LAFTQAL	NLPDV	FGVLVPL	ELKLRIF	RLLDV	RSVLS	SAVCR	360		
Qy	361	DLFTASND	PLLWRFL	YLDRD	FRDNTVR	QD	TWKEL	YRKH	IQKES	PKGRF	VMLLP	SSSTH	420
Db	361	DLFTASND	PLLWRFL	YLDRD	FRDNTVR	QD	TWKEL	YRKH	IQKES	PKGRF	VMLLP	SSSTH	420
Qy	421	TIPFPNPLH	PRPFSS	RLPGI	IGGEYD	QRPTLP	YVGD	PIS	SLIPG	CGET	SPQFP	PLRP	480
Db	421	TIPFPNPLH	PRPFSS	RLPGI	IGGEYD	QRPTLP	YVGD	PIS	SLIPG	CGET	SPQFP	PLRP	480
Qy	481	RFDVGBLP	PGNP	LIP	RGGNDR	PP	PP	PSRGR	PTD	GR	LS	SPM	522
Db	481	RFDVGBLP	PGNP	LIP	RGGNDR	PP	PP	PSRGR	PTD	GR	LS	SPM	522

Query Match: 99.8%; Score 2748; DB 6; Length 522;
Best Local Similarity 99.8%; Pred. No. 5.6e-239;
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLLKRTWPLEVPETPTLGHRLSHLRLSLLLCTWGYSSNTRFTITLNYKDP

Db 1 MRLRVLLKRTWPLEVPETPTLGHRLSHLRLSLLLCTWGYSSNTRFTITLNYKDP

QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSLLQNEQPSLATSSNQTSMQDEQP

Db 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSLLQNEQPSLATSSNQTSMQDEQP

QY 121 SDSFGQAAQSGVWNNDDSMLGPSQNF AEISIQDNAHMAEGTGFYFSEPMLCSESV

Db 121 SDSFGQAAQSGVWNNDDSMLGPSQNF AEISIQDNAHMAEGTGFYFSEPMLCSESV

QY 181 HSLETLYQSA DCSDANDALIVLHLLMLES GVIPQGT EAKALSMPEKWKLSGVYKLYQYMH

Db 181 HSLETLYQSA DCSDANDALIVLHLLMLES GVIPQGT EAKALSMPEKWKLSGVYKLYQYMH

QY 241 PLCEGSSATLTCTVPLGNLIVVNATLKINNEIRSVKRLQLPESFICKEKLGENVANIYKD

Db 241 PLCEGSSATLTCTVPLGNLIVVNATLKINNEIRSVKRLQLPESFICKEKLGENVANIYKD

QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLELKLRIFFRLLDVRSVLS

Db 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLELKLRIFFRLLDVRSVLS

QY 361 DLFTASNDPPLLWRFLYLDRDNTVRQDQDNTWKELYRKHRIQKESPKGRFVMLLP

Db 361 DLFTASNDPPLLWRFLYLDRDNTVRQDQDNTWKELYRKHRIQKESPKGRFVMLLP

QY 421 TIPFPNPLHPRPFSSRLPGIIGGEYDQRPTLPVGDPISSLIIPGCGETSPQFP

Db 421 TIPFPNPLHPRPFSSRLPGIIGGEYDQRPTLPVGDPISSLIIPGCGETSPQFP

QY 481 RPDVPGLPGNPILPGRGPNDRPFRPSRGRPTDGRLSFM

Db 481 RPDVPGLPGNPILPGRGPNDRPFRPSRGRPTDGRLSFM

RESULT 3

ABR47958

ID ABR47958 standard; protein; 522 AA.

XX ABR47958;

AC ABR47958;

XX 12-JUN-2003 (first entry)

DE Human secreted protein, SEQ ID 849.

XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;

KW vulnerary; antiinflammatory; nootropic; neuroprotective;

KW antiparkinsonian; gene therapy; human; cardiovascular disorder.

XX Homo sapiens.

OS

XX WO200295010-A2.

PN

XX 28-NOV-2002.

PD

XX 19-MAR-2002; 2002WO-US009785.

PF

XX 21-MAR-2001; 2001US-0277340P.

PR

XX 19-JUL-2001; 2001US-0306171P.

PR

XX 13-NOV-2001; 2001US-0331287P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX

DR WPI; 2003-129429/12.

XX

PT Novel human secreted proteins, useful for detecting, preventing,

PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular

disorders such as arrhythmia.

Claim 13; SEQ ID NO 849; 1881bp; English.

The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in Alzheimer's disease and Parkinson's neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 522 AA;

Query Match: 99.8%; Score 2748; DB 6; Length 522;													
Best Local Similarity 99.8%; Pred. No. 5.6e-239;													
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0													
Qy	1	MRLRVLLKRTWP	LEVPETETPLGHL	RLSHLRLSL	LLCTWGYSSN	TRFTITLNYK	DP	LTGDE	60				
Db	1	MRLRVLLKRTWP	LEVPETETPLGHL	RLSHLRLSL	LLCTWGYSSN	TRFTITLNYK	DP	LTGDE	60				
Qy	61	ETLASYGIVSGDL	ICLILODDI	PAPNIPSS	TDSHSSLLQ	NEQPSLAT	SSNQTSMQ	DEQP	120				
Db	61	ETLASYGIVSGDL	ICLILODDI	PAPNIPSS	TDSHSSLLQ	NEQPSLAT	SSNQTSMQ	DEQP	120				
Qy	121	SDSFGQAAQSG	VWNNDDSM	LGPSQNF	AEISIQDNA	HMAEGTGF	YFSEPM	LCSESV	EGQVP	180			
Db	121	SDSFGQAAQSG	VWNNDDSM	LGPSQNF	AEISIQDNA	HMAEGTGF	YFSEPM	LCSESV	EGQVP	180			
Qy	181	HSLETLYQSA	DCSDAND	ALIVLH	LLMLES	GVIPQGT	EAKALSM	PEKWKLS	GVYKLY	QYMH	240		
Db	181	HSLETLYQSA	DCSDAND	ALIVLH	LLMLES	GVIPQGT	EAKALSM	PEKWKLS	GVYKLY	QYMH	240		
Qy	241	PLCEGSSAT	LTCTVPL	GNLIVV	NATLKIN	NEIRSV	KRLQLP	ESFICKE	KLGENV	ANIYKD	300		
Db	241	PLCEGSSAT	LTCTVPL	GNLIVV	NATLKIN	NEIRSV	KRLQLP	ESFICKE	KLGENV	ANIYKD	300		
Qy	301	LQKLSRLFK	DQLVYPL	LAFTQAL	NLPDV	FGVLVPL	ELKLRIF	RLLDV	RSVLS	SAVCR	360		
Db	301	LQKLSRLFK	DQLVYPL	LAFTQAL	NLPDV	FGVLVPL	ELKLRIF	RLLDV	RSVLS	SAVCR	360		
Qy	361	DLFTASND	PLLWRFL	YLDRD	FRDNTV	RQD	TWKEL	YRKH	IQKES	PKGRF	VMLLP	SSSTH	420
Db	361	DLFTASND	PLLWRFL	YLDRD	FRDNTV	RQD	TWKEL	YRKH	IQKES	PKGRF	VMLLP	SSSTH	420
Qy	421	TIPFPNPLH	PRPFSS	RLPGI	IGGEYD	QRPTL	PVGD	PIS	SLIPG	CGET	SPQFP	PLRP	480
Db	421	TIPFPNPLH	PRPFSS	RLPGI	IGGEYD	QRPTL	PVGD	PIS	SLIPG	CGET	SPQFP	PLRP	480
Qy	481	RPDPVGLPG	NPILPGR	GPNDRP	FRPSRGR	PTDGR	LSFM	522					
Db	481	RPDPVGLPG	NPILPGR	GPNDRP	FRPSRGR	PTDGR	LSFM	522					

RESULT 4
ABR474366

CC associated F-box protein-lalpha and beta and -2 (SAF-1alpha, SAF-1beta
 CC and SAP-2) and Skp1-associated destruction-box protein (SAD). The
 CC proteins and their coding sequences are useful in the diagnosis and
 CC treatment of cancers, disorders where too little cell division occurs
 CC such as bone marrow aplasia, immunodeficiencies and inflammatory
 CC diseases including sepsis, fibrosis, arthritis and graft versus host
 CC disease
 XX
 XX
 SQ Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 4; Length 522;
 Best Local Similarity 99.6%; Pred. No. 1.3e-238;
 Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
 DB 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
 QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
 DB 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
 QY 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
 DB 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
 QY 181 HSLETLYQSADCSANDALIVLIHLLMLESYGYPQGTAKALSMPEKWLKSGVYKLYQYMH 240
 DB 181 HSLETLYQSADCSANDALIVLIHLLMLESYGYPQGTAKALSMPEKWLKSGVYKLYQYMH 240
 QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
 DB 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
 QY 361 DLFTASNDPLLWRFLYLRDRNTVRVQDTWKELVYKRLHIQRKESPKGRFVMLLPSSSTH 420
 DB 361 DLFTASNDPLLWRFLYLRDRNTVRVQDTWKELVYKRLHIQRKESPKGRFVMLLPSSSTH 420
 QY 421 TTPFYPNPLHPPFPSSRLPGIIGGEVDORTLPGVDPISLLIPGGETSPQFPPLRP 480
 DB 421 TTPFYPNPLHPPFPSSRLPGIIGGEVDORTLPGVDPISLLIPGGETSPQFPPLRP 480
 QY 481 RFDVPGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
 DB 481 RFDVPGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522

RESULT 6
 ABM82342
 ID ABM82342 standard; protein; 522 AA.
 XX
 AC ABM82342;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) polypeptide PRO83271, SEQ.6018.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2004030615-A2.
 XX

PD 15-APR-2004.
 XX 29-SEP-2003; 2003WO-US028547.
 XX
 XX 02-OCT-2002; 2002US-0414971P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Wu TD, Zhang Z, Zhou Y;
 XX WPI; 2004-347921/32.
 DR N-PSDB; ACN40919.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 XX Claim 12; SEQ ID NO 6018; 7273pp; English.
 PS
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 XX Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 8; Length 522;
 Best Local Similarity 99.6%; Pred. No. 1.3e-238;
 Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
 DB 1 MRLRVLRLKRTWPLEVPETPTLGLHRLSHLRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
 QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
 DB 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
 QY 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
 DB 121 SDSFOGQAQAGVWDDSMGLGFSQNFEAESIODNAHMAEGTGYFSEPMLCSESVEGQVP 180
 QY 181 HSLETLYQSADCSANDALIVLIHLLMLESYGYPQGTAKALSMPEKWLKSGVYKLYQYMH 240
 DB 181 HSLETLYQSADCSANDALIVLIHLLMLESYGYPQGTAKALSMPEKWLKSGVYKLYQYMH 240
 QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
 DB 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
 QY 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVGVLVPLPLEKLIIFRLLDVRSVLISAVCR 360
 DB 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVGVLVPLPLEKLIIFRLLDVRSVLISAVCR 360
 QY 361 DLFTASNDPLLWRFLYLRDRNTVRVQDTWKELVYKRLHIQRKESPKGRFVMLLPSSSTH 420
 DB 361 DLFTASNDPLLWRFLYLRDRNTVRVQDTWKELVYKRLHIQRKESPKGRFVMLLPSSSTH 420

Db	361	DLFTASNDPLLWRFYLRLDRDNTVRVQDTWKELYRKRHQKESPKGRFVMLLPSSTH	420
Qy	421	TIPPEVNPPLHPRPSSRLPPGIIIGEYDQRTPLPVGDPISLLIPGGETSQPPPLRP	480
Db	421	TIPFPNPPLHPRPFPSSRLPPGIIIGEYDQRTPLPVGDPISLLIPGGETSQPPPLRP	480
Qy	481	REDPVGPLPGPNPLPGRGPNDRPFPFRSRRGPTDGRLSFM	522
Db	481	REDPVGPLPGPNPLPGRGPNDRPFPFRSRRGPTDGRLSFM	522
RESULT 7			
AAW68521	AAW68521 standard; protein; 591 AA.		
XX	AC	AAW68521;	
XX	DT	25-JAN-1999 (first entry)	
XX	DE	Human RIP-associated protein.	
XX	XX	Human; RIP-associated protein; RAP; primer; PCR; amplification; probe; hybridisation; death domain; MORT MODULE; ICE-like family protease; kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.	
OS	XX	Homo sapiens.	
XX	XX	WO9841624-A1.	
PN	XX	24-SEP-1998.	
XX	XX	19-MAR-1998; 98WO-IL000125.	
PF	XX	19-MAR-1997; 97IL-00120485.	
PR	XX	(YEDA) YEDA RES & DEV CO LTD.	
PA	XX	Wallach D, Kovalenko A;	
PI	XX	WPI: 1998-531565/45.	
XX	XX	N-PSDB; AAV57200.	
DR	XX	DNA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of tumour cells or HIV-infected cells.	
PT	XX	Claim 10; Fig 2; 65pp; English.	
PS	XX	This sequence represent part of a human RIP-associated protein (RAP). The coding sequence was isolated from a B-cell library by a yeast 2-hybrid screen using the RIP protein devoid of its "death domain" as a bait. The screen isolated a clone of about 1.9 kb. Primers were generated based on the sequence and used to PCR amplify probes for screening a colon and heart cDNA library. A further 300 bp of sequence was determined, which was added to the 1.9 kb of sequence from the B-cell library. The encoded protein does not contain a "death domain", MORT MODULE, ICE-like family protease domain, kinase domain, nor TRAF domains. RAP was shown to bind only to RIP and not to TRADD, MORT-1, p55-R, p75-R or MACH. The protein can be used to modulate or mediate RIP modulated/mediated intracellular effects on the inflammation, cell death or cell survival pathways in which RIP is involved, e.g. for treating tumour cells or HIV-infected cells	
XX	XX	Sequence 591 AA;	
Qy	Query Match 91.1%; Score 2510; DB 2; Length 591; Best Local Similarity 99.6%; Pred. No. 2.2e-217; Matches 479; Conservative 0; Mismatches 0; Indels 2; Gaps 1;		
Qy	42	SNTRFTITLNYKDLTGDETLASGYIVSGDILICILQDDIPAPNIPSTDSEHSLQNN	101
Db	113	SNTRFTITLNYKDLTGDETLASGYIVSGDILICILQDDIPAPNIPSTDSEHSLQNN	172
Qy	102	EQPSLATSSNOTSMQDEQSDSFQGAQAQSGVWNNDSMLGPSQNFEAESIQNAHMAECT	161

Db	173	EQ--LATSSNOTSMQDEQSDSFQGAQAQSGVWNNDSMLGPSQNFEAESIQNAHMAECT	230
Qy	162	GFYPSEPMLCSESVEGQVPHSLLETLYQSADCSANDALIVLHLLMLESGYIPOGTEAKA	221
Db	231	GFYPSEPMLCSESVEGQVPHSLLETLYQSADCSANDALIVLHLLMLESGYIPOGTEAKA	290
Qy	222	LSMPEKWKLSGVYKLOYMHPICEGSSATLTCVPLGNLIWVNATLKINNEIRSVKRLQLLP	281
Db	291	LSMPEKWKLSGVYKLOYMHPICEGSSATLTCVPLGNLIWVNATLKINNEIRSVKRLQLLP	350
Qy	282	ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTRAQLNLPDVFGLVVLPLEKL	341
Db	351	ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTRAQLNLPDVFGLVVLPLEKL	410
Qy	342	RIFRLLDVRSVLISAVCRDLFTASNDPILWRFYLRLDRDNTVRVQDTWKELYRKHI	401
Db	411	RIFRLLDVRSVLISAVCRDLFTASNDPILWRFYLRLDRDNTVRVQDTWKELYRKHI	470
Qy	402	QRKESPKGRFVMLLPSSSTHTTIPFVNPPLHPRPFPSSRLPPGIIIGEYDQRTPLPVGDDP	461
Db	471	QRKESPKGRFVMLLPSSSTHTTIPFVNPPLHPRPFPSSRLPPGIIIGEYDQRTPLPVGDDP	530
Qy	462	SSLIPGGETSQPPPLPRPFPDPVGPLPGPNPILPGRGPNDRPFPFRSRRGPTDGRLSF	521
Db	531	SSLIPGGETSQPPPLPRPFPDPVGPLPGPNPILPGRGPNDRPFPFRSRRGPTDGRLSF	590
Qy	522	M 522	
Db	591	M 591	
RESULT 8			
AAW83047	AAW83047 standard; protein; 482 AA.		
XX	AC	AAW83047;	
XX	DT	16-AUG-2000 (first entry)	
XX	DE	F-box protein FBP-7.	
XX	XX	F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist; proliferative disorder; differentiative disorder; breast cancer; prostate cancer; ovarian cancer; cancer; small cell lung carcinoma; immune disorder; cardiovascular disorder; inflammatory disorder; human.	
OS	XX	Homo sapiens.	
XX	XX	WO200012679-A1.	
XX	PD	09-MAR-2000.	
XX	PF	27-AUG-1999; 99WO-US019560.	
XX	PR	28-AUG-1998; 98US-0098355P.	
XX	PR	03-FEB-1999; 99US-0118568P.	
XX	PR	15-MAR-1999; 99US-0124449P.	
XX	PA	(UYNY) UNIV NEW YORK STATE.	
XX	PI	Chiaur DS, Pagano M, Latres E;	
XX	DR	WPI: 2000-256635/22.	
XX	DR	N-PSDB; AAZ93356.	
XX	PT	Novel nucleic acid for screening compounds useful for treating proliferative and differentiative disorders such as cancer and immune disorders comprises sequences encoding ubiquitin ligases.	
XX	PS	Claim 10; Fig 10a; 245pp; English.	
XX	CC	Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases	

Db 482 M 482

RESULT 10

AAU32109

ID AAU32109 standard; protein., 607 AA.

XX AC AAU32109;

XX DT 18-DEC-2001 (first entry)

XX DE

XX DE Novel human secreted protein #2600.

XX KW Human; vaccination; gene therapy; nutritional supplement;

XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US008656.

XX PR 18-APR-2000; 2000US-00552929.

XX PR 26-JAN-2001; 2001US-00770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic

XX PT vaccination, testing and therapy.

XX PS Claim 20; Page 556; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The

XX CC polypeptides and antibodies to the polypeptides are useful for

XX CC determining the presence of or predisposition to a disease associated

XX CC with altered levels of polypeptide. The polypeptides are also useful for

XX CC identifying agents (agonists and antagonists) that bind to them. Cells

XX CC expressing the proteins are useful for identifying a therapeutic agent

XX CC for use in treatment of a pathology related to aberrant expression or

XX CC physiological interactions of the polypeptide. Vectors comprising the

XX CC nucleic acids encoding the polypeptides and cells genetically engineered

XX CC to express them are also useful for producing the proteins. The proteins

XX CC are useful in genetic vaccination, testing and therapy, and can be used

XX CC as nutritional supplements. They may be used to increase stem cell

XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon

XX CC and/or nerve tissue growth or regeneration; immune suppression and/or

XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human

XX CC secreted proteins of the invention

XX SQ Sequence 607 AA;

Query Match 88.9%; Score 2448.5; DB 4; Length 607;

Best Local Similarity 90.8%; Pred. No. 8.3e-212;

Matches 481; Conservative 7; Mismatches 33; Indels 9; Gaps 5;

QY 1 MLRLVRLKRTWPLEVPEPETEPTGLHRLSHRLSLILCTWGYSSNTRFTITLNYKDLTGDE 60

DB 36 MLRLVRLKRTWPLEVPEPETEPTGLHRLSHRLSLILCTWGYSSNTRFTITLNYKDLTGDE 95

QY 61 ETLASVIGVSGDLICILIQDDIPAPNIPSSDSEHSSIQNNQPSLATSSNQTSMQDQOP 120

DB 96 ETLASVIGVSGDLICILIQDDIPAPNIPSSDSEHSSIQNNQPSLATSSNQTSMQDQOP 155

QY 121 SDSFOGQAQSGVWDDSLMGLPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 180

Db 156 SDSFOGQAQSGVWDDSLMGLPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 215

QY 181 HSLETLYOSADCSANDALIVLIHLLMLESYIPOGTEAKALSMPEKWKLSGVYKLYMH 240

Db 216 HSLETLYOSADCSANDALIVLIHLLMLESYIPOGTEAKALSMPEKWKLSGVYKLYMH 275

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300

Db 276 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 335

QY 301 LOKLSRFLKQOLVYPLLAFTQALNLPDVFGLVLPLELKLRIFRLLDVRSVLSAVCR 360

Db 336 LQKLSRFLKQOLVYPLLAFTQALNLPDVFGLVLPLELKLRIFRLLDVRSVLSAVCR 395

QY 361 DLFTASNDPLLRFLYLRDFRNTVRVODTDWKELYKRKHQKESPKGRFVMLLPSSSTH 420

Db 396 DLFTASNDPLLRFLYLRDFRNTVRVODTDWKELYKRKHQKESPKGRFVMLLPSSSTH 455

QY 421 TIFYPNPLHPRFPSSRLPGIIGGEYDORP-TLPYVVDPISSLIPOG-GETPS-QFPP 477

Db 456 TIFYPNPLHPRFPSSRLPGIIGGEYDPTNTFPMGLDPISSLIPMVLGETPQSPFP 515

QY 478 -----LRPRFDPVGLPGFNPIPGRGGNDRFPFRPSRGRPTDGRLSFM 522

Db 516 TETHALNPSPPIGRDNPQSCPGAEGGPNRTRFPPLRPOP-GGRANLM 564

RESULT 11

ABB90109

ID ABB90109 standard; protein; 462 AA.

XX AC ABB90109;

XX DT 24-MAY-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 2485.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

XX KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

XX KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;

XX KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;

XX KW neurological disease; infection; human; secreted protein.

XX OS Homo sapiens.

XX PN WO200190304-A2.

XX PD 29-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016450.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX DR WPI; 2002-122018/16.

XX DR N-PSDB; ABL90518.

XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and

XX PT prevention of neural, immune system, muscular, reproductive,

XX PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative

XX PT disorders.

XX PS Claim 11; SEQ ID NO 2485; 2081pp + Sequence Listing; English.

XX CC The invention relates to novel genes (ABL89449-ABL90853) and proteins

XX CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating

XX CC medical conditions e.g. by protein or gene therapy. The genes are

XX CC isolated from a range of human tissues disclosed in the specification.

XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 5; Length 462;
Best Local Similarity 88.1%; Pred. No. 5.8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
QY 1 MRLRVLRLKRTWPLEVPEPETPTLGLHRLSHLRSLLLCTWGYSSNTFTITLNYKDPDLTGDE 60
DB 1 MRLRVLRLKRTWPLEVPEPETPTLGLHRLSHLRSLLLCTWGYSSNTFTITLNYKDPDLTGDE 60
QY 61 ETLASGVISGDLICLLIQLDDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQWDEQP 120
DB 61 ETLASGVISGDLICLLIQLDDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQWDEQP 120
QY 121 SDSFOGQAQSGVNDSDMLGFSQNFPEABSIQDNAMHAEGTGFPSEPMLCSESVEGQVP 180
DB 121 SDSFOGQAQSGVNDSDMLGFSQNFPEABSIQDNAMHAEGTGFPSEPMLCSESVEGQVP 180
QY 181 HSLETLYSADCSNDALIVLHLMLESYVPOGTEAKALSMPEKWLKGVYKLYQYMH 240
DB 181 HSLETLYSADCSNDALIVLHLMLESYVPOGTEAKALSMPEKWLKGVYKLYQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVN----- 262
QY 301 LQKLSRLFKDQLVYPLLAFTROALNPDVFLGLWLPLEKLKIFRLLDVRSVLSSAVCR 360
DB 263 -----ALNLPDVFGLVPLLEKLKIFRLLDVRSVLSSAVCR 300
QY 361 DLFTASNDPLLRFLYLRDRDNTVRVQTDWKELYRKRHIOKESPKGRFVWMLPSSTH 420
DB 301 DLFTASNDPLLRFLYLRDRDNTVRVQTDWKELYRKRHIOKESPKGRFVWMLPSSTH 360
QY 421 TIFPYNPLHPPFPSSRLPPGIIGGEVDORTLTPYVGDPISSLIPGGETPSQPPPLRP 480
DB 361 TIFPYNPLHPPFPSSRLPPGIIGGEVDORTLTPYVGDPISSLIPGGETPSQPPPLRP 420
QY 481 RPDVPGLPGNPILPGRGGPNDRPFRPSRCRPTDGRLSFM 522
DB 421 RPDVPGLPGNPILPGRGGPNDRPFRPSRCRPTDGRLSFM 462

RESULT 12
ID ADAS7586 standard; protein; 462 AA.
XX ADAS7586;
AC ADAS7586;
XX
DT 20-NOV-2003 (first entry)
XX
XX Human secreted protein #566.
DE
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;

KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX Homo sapiens.
OS WO2002102994-A2.
PN 27-DEC-2002.
PD 19-MAR-2002; 2002WO-US008278.
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
PI WPI; 2003-167512/16.
XX N-PSDB; ADA56693.
DR New human secreted polypeptides and polynucleotides, useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX Claim 13; SEQ ID NO 1779; 1754pp; English.
PS The invention relates to 592 new human secreted polypeptides useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy) cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 6; Length 462;
Best Local Similarity 88.1%; Pred. No. 5.8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
QY 1 MRLRVLRLKRTWPLEVPEPETPTLGLHRLSHLRSLLLCTWGYSSNTFTITLNYKDPDLTGDE 60
DB 1 MRLRVLRLKRTWPLEVPEPETPTLGLHRLSHLRSLLLCTWGYSSNTFTITLNYKDPDLTGDE 60
QY 61 ETLASGVISGDLICLLIQLDDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQWDEQP 120
DB 61 ETLASGVISGDLICLLIQLDDIPAPNIPSSDTSEHSSLQNNQPSLATSSNOTSQWDEQP 120

QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFYSEPMCLCSSEVGGQVP 180
Db |||||
QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFYSEPMCLCSSEVGGQVP 180
Db |||||
QY 181 HSLETLYQSADCSNDALIVLIHLLMLESYIPQTEAKALSMPEKWKLSGVYKLYQYMH 240
Db |||||
QY 181 HSLETLYQSADCSNDALIVLIHLLMLESYIPQTEAKALSMPEKWKLSGVYKLYQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
Db |||||
QY 241 PLCEGSSATLTCVPLGNLIVVN----- 262
QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 360
Db -----ALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 300
QY 361 DLFTASNDPDLWRFLYLRDPRDNTVRVQDQTEAKALSMPEKWKLSGVYKLYQYMH 420
Db |||||
QY 301 DLFTASNDPDLWRFLYLRDPRDNTVRVQDQTEAKALSMPEKWKLSGVYKLYQYMH 360
QY 421 TIPFPVNLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 480
Db |||||
QY 361 TIPFPVNLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 420
QY 481 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
Db |||||
QY 421 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 13
ADA41482
ID ADA41482 standard; protein; 462 AA.
XX
AC ADA41482;
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein.
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnary; cardiant; gene therapy.
XX
OS Homo sapiens.
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI; 2003-175238/17.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1865; 3205pp; English.
XX
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC

CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), infectious diseases (bacterial,
CC e.g. atherosclerosis, myocarditis), cardiovascular disorders (e.g.
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 6; Length 462;
Best Local Similarity 88.1%; Pred. No. 5.8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
QY 1 MRLRVLLKRTWPLEVPEPETLGHLSRLSLLLCTGWGYSNTRFTTILNYKDLPTGDE 60
Db |||||
QY 1 MRLRVLLKRTWPLEVPEPETLGHLSRLSLLLCTGWGYSNTRFTTILNYKDLPTGDE 60
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDTSSEHSSLQNNQPSLATSSNQTSMQDEOP 120
Db |||||
QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDTSSEHSSLQNNQPSLATSSNQTSMQDEOP 120
QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFYSEPMCLCSSEVGGQVP 180
Db |||||
QY 121 SDSFGQAAQSGVWDDSMGLGSPQNFSESIQDNAMHAEAGTGFYSEPMCLCSSEVGGQVP 180
QY 181 HSLETLYQSADCSNDALIVLIHLLMLESYIPQTEAKALSMPEKWKLSGVYKLYQYMH 240
Db |||||
QY 181 HSLETLYQSADCSNDALIVLIHLLMLESYIPQTEAKALSMPEKWKLSGVYKLYQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300
Db |||||
QY 241 PLCEGSSATLTCVPLGNLIVVN----- 262
QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 360
Db -----ALNLPDVFGVLVPLLEKLRIFFRLDVRSVLSAVCR 300
QY 361 DLFTASNDPDLWRFLYLRDPRDNTVRVQDQTEAKALSMPEKWKLSGVYKLYQYMH 420
Db |||||
QY 301 DLFTASNDPDLWRFLYLRDPRDNTVRVQDQTEAKALSMPEKWKLSGVYKLYQYMH 360
QY 421 TIPFPVNLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 480
Db |||||
QY 361 TIPFPVNLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPISLLIPGCGTSPQFPPLRP 420
QY 481 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
Db |||||
QY 421 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462
RESULT 14
ABR48139
ID ABR48139 standard; protein; 462 AA.

XX AC ABR48139;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human secreted protein, SEQ ID 1030.
 XX KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
 KW vulnerable; antiinflammatory; neurotropic; neuroprotective;
 KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
 XX OS Homo sapiens.
 XX PN WO200295010-A2.
 XX PD 28-NOV-2002.
 XX PF 19-MAR-2002; 2002WO-US009785.
 XX PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX DR WPI; 2003-129429/12.
 XX PT Novel human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 PT disorders such as arrhythmia.
 XX PS Claim 13; SEQ ID NO 1030; 1881pp; English.
 XX CC The present invention relates to novel human secreted proteins (ABR47633-
 CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
 CC and their coding sequences are useful for the preparation of a diagnostic
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular
 CC disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,
 CC proliferative disorders and/or cancerous diseases and conditions, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural damage which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts, to prevent skin aging or hair loss, to
 CC stimulate growth and differentiation of haematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines, to maintain
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues, to increase or decrease differentiation or proliferation of
 CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism. Note: The sequence data for this patent was published in
 CC electronic format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 462 AA;
 Query Match 87.3%; Score 2404; DB 6; Length 462;
 Best Local Similarity 88.1%; Pred. No. 5.8e-208;
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
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 QY 421 TIFYPNPLHPRPFPSSRLPGIIGGEYDQRTPLPYVGDPISLIPGGETPSQFPPLRP 480
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 ID ADC74596 standard; protein; 462 AA.
 XX AC ADC74596;
 XX DT 01-JAN-2004 (first entry)
 XX DE Human secreted protein - SEQ ID 1229.
 KW antinaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 KW antidiabetic; immunosuppressive; dermatological; nephrotropic;
 KW antiparkinsonian; neuroprotective; neurotropic; antibacterial; virucide;
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnery; cytostatic;
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
 KW human.
 XX OS Homo sapiens.
 XX PN WO2003038063-A2.
 XX PD 08-MAY-2003.
 XX PF 19-MAR-2002; 2002WO-US008277.
 XX PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX DR WPI; 2003-430516/40.
 DR N-ESDB; ADC73981.
 XX PT New human secreted polypeptide for diagnosing, preventing or treating
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 PT atherosclerosis).


```

XX Claim 16; SEQ ID NO 1229; 2272pp; English.
PS
XX
CC The invention relates to a novel human secreted polypeptide comprising a
CC defined sequence given in the specification. The polypeptide, nucleic
CC acid molecule, antibody, agonist or antagonist of the invention may be
CC useful for preparing a composition for diagnosing or treating a
CC haemopoietic or haematologic disorder such as anaemia, autoimmune
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC diabetes, systemic lupus erythematosus or glomerulonephritis,
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC disease, wounds and hyperproliferative disorders including
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC parasitic infections. The polypeptide may also be used during gene
CC therapy procedures and for identifying a binding partner by contacting
CC the polypeptide with a binding partner and determining whether the
CC binding partner increases or decreases the activity of the polypeptide.
CC The current sequence is that of the human secreted protein of the
CC invention.
XX
SQ Sequence 462 AA;
Query Match 87.3%; Score 2404; DB 7; Length 462;
Best Local Similarity 88.1%; Pred. No. 5.8e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
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Job time : 170 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:19:59 ; Search time 161 Seconds
(without alignments)
1258.598 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 3818149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2754	100.0	522	14	US-10-245-593-2
3	2744	99.6	522	16	US-10-679-246-10
4	2489	90.4	482	13	US-10-042-417-14
5	2489	90.4	482	17	US-10-652-928-14
6	2404	87.3	462	10	US-09-397-945-200
7	2404	87.3	462	15	US-10-264-237-2485
8	2404	87.3	462	15	US-10-653-595-200
9	2404	87.3	497	10	US-09-397-945-435
10	2404	87.3	497	15	US-10-653-595-435
11	2270	82.4	443	16	US-10-679-246-8

12	1527	55.4	317	15	US-10-264-237-2484	Sequence 2484, Ap
13	1238	45.0	231	16	US-10-408-765A-752	Sequence 752, App
14	1086	33.4	221	15	US-10-094-749-1723	Sequence 1723, Ap
15	714	25.9	174	10	US-09-397-945-434	Sequence 434, App
16	714	25.9	174	15	US-10-653-595-209	Sequence 209, App
17	714	25.9	174	15	US-10-653-595-434	Sequence 434, App
18	714	25.9	175	10	US-09-397-945-209	Sequence 209, App
19	396	14.4	76	14	US-10-029-386-27908	Sequence 27908, A
20	249	9.0	47	14	US-10-029-386-33496	Sequence 33496, A
21	215.5	7.8	500	16	US-10-739-930-3910	Sequence 9910, A
22	211	7.7	485	15	US-10-425-114-59110	Sequence 59110, A
23	207	7.5	485	15	US-10-425-114-59111	Sequence 59111, A
24	201	7.3	485	15	US-10-425-114-60984	Sequence 60984, A
25	198	7.0	447	16	US-10-425-115-349540	Sequence 349540,
26	194	7.0	39	13	US-10-042-417-21	Sequence 21, Appl
27	194	7.0	39	17	US-10-652-928-21	Sequence 21, Appl
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30	144	5.2	408	15	US-10-264-237-1835	Sequence 1835, Ap
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33	139	5.0	327	13	US-10-042-417-58	Sequence 58, Appl
34	139	5.0	327	16	US-10-679-246-12	Sequence 12, Appl
35	139	5.0	327	17	US-10-652-928-58	Sequence 58, Appl
36	137	5.0	664	16	US-10-437-963-176808	Sequence 176808,
37	129.5	4.7	197	16	US-10-425-115-356769	Sequence 356769,
38	128.5	4.7	842	17	US-10-732-923-13573	Sequence 13573, A
39	128.5	4.7	850	17	US-10-732-923-13572	Sequence 13572, A
40	126	4.6	344	14	US-10-061-043A-27	Sequence 27, Appl
41	126	4.6	344	15	US-10-060-634C-27	Sequence 27, Appl
42	126	4.6	355	14	US-10-061-043A-35	Sequence 35, Appl
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44	126	4.6	355	15	US-10-094-749-2883	Sequence 2883, Ap
45	125.5	4.6	754	16	US-10-437-963-134895	Sequence 134895,

ALIGNMENTS

RESULT 1
US-09-927-458-2
; Sequence 2, Application US/09927458
; Patent No. US20020058024A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
; TITLE OF INVENTION: AND OTHER PROTEINS
; FILE REFERENCE: WALLACH-22A
; CURRENT APPLICATION NUMBER: US/09/927,458
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/IL98/00125
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: IL 120485
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: 09/381,358
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-458-2

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RESULT 2
US-10-245-593-2
; Sequence 2, Application US/10245593
; Publication No. US2003039646A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR F
; FILE REFERENCE: WALLACH=22A
; CURRENT APPLICATION NUMBER: US/10/245,593
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/927,458
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/IL98/00125
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: IL 120485
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: 09/381,358
; PRIOR FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-593-2

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Best Local Similarity 100.0%; Pred. No. 2,4e-223;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-10-679-246-10
; Sequence 10, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: in Protein Degradation, Products and Methods Related Thereo
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-10

Query Match 99.6%; Score 2744; DB 16; Length 522;
Best Local Similarity 99.6%; Pred. No. 1.7e-222;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4
US-10-042-417-14
; Sequence 14, Application US/10042417
; Publication No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; Proliferative and Differentiative Disorders
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-5
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-14

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Best Local Similarity 98.1%; Pred. No. 5.1e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 222 LSMPEKWLKSGVYKQYMHPLCEGSSATLTCVPLGNLIWVATLKNNEIRSVKRLQLLP 281
Db 122 GYPSEPLLCSSVEGQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 181
QY 282 ESFICKEKLGENVANIYKDQKLSRLFKDQVYPLLATRQALNLPDVFGVLVPLLEKL 341
Db 182 LSLPEKWLKSGVYKQYMHPLCEGSSATLTCVPLGNLIWVATLKNNEIRSVKRLQLLP 241
QY 342 RIFRLDVRVLSLSAVCRDLFTASNDPLLRFLYLRDFRNTVRVQTDWKELYRKHI 401
Db 242 ESFICKEKLGENVANIYKDQKLSRLFKDQVYPLLATRQALNLPDVFGVLVPLLEKL 301
QY 402 RQKESPKGRFVMLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGGEYDQRTPLPYVGDPI 461
Db 362 RQKESPKGRFVMLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGGEYDQRTPLPYVGDPI 421
QY 462 SSLIFPGGETPSQFPPLRPDPVGPLPGNPILPGRGPNDRFPFRSRGRPTDGRLSF 521

Db 422 SSLIFPGGETPSQFPPLRPDPVGPLPGNPILPGRGPNDRFPFRSRGRPTDGRLSF 481
QY 522 M 522
Db 482 M 482

RESULT 5
US-10-652-928-14
; Sequence 14, Application US/10652928
; Publication No. US20050079558A1
; GENERAL INFORMATION:
; APPLICANT: Chaiur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/652,928
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-928-14

Query Match 90.4%; Score 2489; DB 17; Length 482;
Best Local Similarity 98.1%; Pred. No. 5.1e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 42 SNTRFTITLNYKDPITGDETLASVIGSDGLICILIQDDIPAPNIPSTDSHSSLQNN 101
Db 2 SNTRFTITLNYKDPITGDETLASVIGSDGLICILIQDDIPAPNIPSTDSHSSLQNN 61
QY 102 EQPSLATSSNOTSMODEPSDFSQQAQSGVWVNDSDMLGPSONFEAESIQDNAHMAEGT 161
Db 62 EQPSLATSSNOTSIQDEQPSDFSQQAQSGVWVNDSDMLGPSONFEAESIQDNAHMAEGT 121
QY 162 GYPSEPMLCSSVEGQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 221
Db 122 GYPSEPLLCSSVEGQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 181
QY 222 LSMPEKWLKSGVYKQYMHPLCEGSSATLTCVPLGNLIWVATLKNNEIRSVKRLQLLP 281
Db 122 GYPSEPLLCSSVEGQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKA 181
QY 282 ESFICKEKLGENVANIYKDQKLSRLFKDQVYPLLATRQALNLPDVFGVLVPLLEKL 341
Db 242 ESFICKEKLGENVANIYKDQKLSRLFKDQVYPLLATRQALNLPDVFGVLVPLLEKL 301
QY 342 RIFRLDVRVLSLSAVCRDLFTASNDPLLRFLYLRDFRNTVRVQTDWKELYRKHI 401
Db 302 RIFRLDVRVLSLSAVCRDLFTASNDPLLRFLYLRDFRNTVRVQTDWKELYRKHI 361
QY 402 RQKESPKGRFVMLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGGEYDQRTPLPYVGDPI 461
Db 362 RQKESPKGRFVMLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGGEYDQRTPLPYVGDPI 421
QY 462 SSLIFPGGETPSQFPPLRPDPVGPLPGNPILPGRGPNDRFPFRSRGRPTDGRLSF 521
Db 422 SSLIFPGGETPSQFPPLRPDPVGPLPGNPILPGRGPNDRFPFRSRGRPTDGRLSF 481
QY 522 M 522

Db 482 M 482

RESULT 6

US-09-397-945-200

; Sequence 200, Application US/09397945

; Publication No. US20030065139A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: 95 Human secreted proteins

; FILE REFERENCE: P2027P1

; CURRENT APPLICATION NUMBER: US/09/397,945

; CURRENT FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/05804

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,566

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,576

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,573

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,574

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,579

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,314

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080,312

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/078,578

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,581

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,577

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,563

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,313

; PRIOR FILING DATE: 1998-04-01

; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 200

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (115)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-397-945-200

Query Match 87.3%; Score 2404; DB 10; Length 462;

Best Local Similarity 88.1%; Pred. No. 7.1e-194;

Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPETETLGHLSRLSLCTGWGSSNTRFTITLNYKDLPTGDE 60

Db 1 MRLRVLLKRTWPLEVPETETLGHLSRLSLCTGWGSSNTRFTITLNYKDLPTGDE 60

QY 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120

Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120

QY 121 SDSFGQAAQSGVWDDSMGLGFSQNFESIQDNNAHMAEGTGYFSEPMLCSESVEGQVP 180

Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120

QY 121 SDSFGQAAQSGVWDDSMGLGFSQNFESIQDNNAHMAEGTGYFSEPMLCSESVEGQVP 180

QY 181 HSLETLYOSADCSDDANDALIVLIHLLMESGYIPGTEAKALSMPEKWKLSGVYKLOYMH 240

Db 181 HSLETLYOSADCSDDANDALIVLIHLLMESGYIPGTEAKALSMPEKWKLSGVYKLOYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300

Db 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300

Db 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300

QY 301 LQKLSRLFKDQIVVPLLAFTQALNLPDVFGVLVPLLELKLRIFFLLDVRSVLSAVCR 360

Db 263 -----ALNLPDVFGVLVPLLELKLRIFFLLDVRSVLSAVCR 300

QY 361 DLFTASNDPLLWRFLYLDRFRDNTVRVQDQDQPTLPGYVGDPISSSLIPGCGTETSPQPPPLRP 480

Db 301 DLFTASNDPLLWRFLYLDRFRDNTVRVQDQDQPTLPGYVGDPISSSLIPGCGTETSPQPPPLRP 480

QY 421 TIPFYPNLHPRPPFPSSRLPPGIIIGGEYDQDQPTLPGYVGDPISSSLIPGCGTETSPQPPPLRP 420

Db 361 TIPFYPNLHPRPPFPSSRLPPGIIIGGEYDQDQPTLPGYVGDPISSSLIPGCGTETSPQPPPLRP 420

QY 481 RPDVGPPLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 522

Db 421 RPDVGPPLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 462

RESULT 7

US-10-264-237-2485

; Sequence 2485, Application US/10264237

; Publication No. US20040009491A1

; GENERAL INFORMATION:

; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA131PI

; CURRENT APPLICATION NUMBER: US/10/264,237

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/16450

; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/205,515

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 2876

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 2485

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (115)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-237-2485

Query Match 87.3%; Score 2404; DB 15; Length 462;

Best Local Similarity 88.1%; Pred. No. 7.1e-194;

Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPETETLGHLSRLSLCTGWGSSNTRFTITLNYKDLPTGDE 60

Db 1 MRLRVLLKRTWPLEVPETETLGHLSRLSLCTGWGSSNTRFTITLNYKDLPTGDE 60

QY 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120

Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120

QY 121 SDSFGQAAQSGVWDDSMGLGFSQNFESIQDNNAHMAEGTGYFSEPMLCSESVEGQVP 180

Db 121 SDSFGQAAQSGVWDDSMGLGFSQNFESIQDNNAHMAEGTGYFSEPMLCSESVEGQVP 180

QY 181 HSLETLYOSADCSDDANDALIVLIHLLMESGYIPGTEAKALSMPEKWKLSGVYKLOYMH 240

Db 181 HSLETLYOSADCSDDANDALIVLIHLLMESGYIPGTEAKALSMPEKWKLSGVYKLOYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300

Db 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300

QY 301 LQKLSRLFKDQIVVPLLAFTQALNLPDVFGVLVPLLELKLRIFFLLDVRSVLSAVCR 360

Db 263 -----ALNLPDVFGVLVPLLELKLRIFFLLDVRSVLSAVCR 300

QY 361 DLFTASNDPLLRFLYLRDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 420
DB 301 DLFTASNDPLLRFLYLRDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 360
QY 421 TIPFPNPLHPRPFPSSRLPGIIGGEYDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 480
DB 361 TIPFPNPLHPRPFPSSRLPGIIGGEYDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 420
QY 481 RFDVGPPLGPNPILPGRGPNDRPFPSPRGRPTDGRLSFM 522
DB 421 RFDVGPPLGPNPILPGRGPNDRPFPSPRGRPTDGRLSFM 462

RESULT 8

US-10-653-595-200
; Sequence 200, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.

; TITLE OF INVENTION: 95 Human secreted proteins

; FILE REFERENCE: PZ027P1C1

; CURRENT APPLICATION NUMBER: US/10/653.595

; CURRENT FILING DATE: 2003-09-03

; PRIOR APPLICATION NUMBER: US 09/397945

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/05804

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,566

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,576

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,573

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,574

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,579

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,314

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080,312

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/078,578

; PRIOR FILING DATE: 1998-03-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 200

; LENGTH: 462

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (115)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-653-595-200

Query Match

Best Local Similarity 87.3%; Score 2404; DB 15; Length 462;

Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLRLKRTWPLVPEPTGLHRLSHRLSLICTWGYSSNTRFTITLNYKDLTGDE 60

DB 1 MRLRVLRLKRTWPLVPEPTGLHRLSHRLSLICTWGYSSNTRFTITLNYKDLTGDE 60

QY 61 ETLASVGVISGDLICLLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNOTSMDQEP 120

DB 61 ETLASVGVISGDLICLLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNOTSMDQEP 120

QY 121 SDSFGQAAQAGVWDDSMGLGSPQNFQESIQDNHMAEGTGYFSEPMLCSEVGGQVP 180

DB 121 SDSFGQAAQAGVWDDSMGLGSPQNFQESIQDNHMAEGTGYFSEPMLCSEVGGQVP 180

QY 181 HSLETLYOSADCSANDALIVLIHLLMLESYVPOGTEAKALSMPEKWKLSGVYKLOYMH 240
DB 181 HSLETLYOSADCSANDALIVLIHLLMLESYVPOGTEAKALSMPEKWKLSGVYKLOYMH 240
QY 241 PLCGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESFTCKEKLGENVANIYKD 300
DB 241 PLCGSSATLTCVPLGNLIVN----- 262
QY 301 LOKLSRLPKDQVPLVPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 360
DB 263 -----ALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 300
QY 361 DLFTASNDPLLRFLYLRDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 420
DB 301 DLFTASNDPLLRFLYLRDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 360
QY 421 TIPFPNPLHPRPFPSSRLPGIIGGEYDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 480
DB 361 TIPFPNPLHPRPFPSSRLPGIIGGEYDQRTVQDTWKELRYRKHIOKESPKGRFVMLLPSSSTH 420
QY 481 RFDVGPPLGPNPILPGRGPNDRPFPSPRGRPTDGRLSFM 522
DB 421 RFDVGPPLGPNPILPGRGPNDRPFPSPRGRPTDGRLSFM 462

RESULT 9

US-09-397-945-435

; Sequence 435, Application US/09397945

; Publication No. US20030065139A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: 95 Human secreted proteins

; FILE REFERENCE: PZ027P1

; CURRENT APPLICATION NUMBER: US/09/397,945

; CURRENT FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/05804

; PRIOR FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: 60/078,566

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,576

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,573

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,574

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,579

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,314

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/080,312

; PRIOR FILING DATE: 1998-04-01

; PRIOR APPLICATION NUMBER: 60/078,578

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,581

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,577

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,563

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/080,313

; PRIOR FILING DATE: 1998-04-01

; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 435

; LENGTH: 497

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (150)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-397-945-435

Query Match 87.3%; Score 2404; DB 10; Length 497;
Best Local Similarity 88.1%; Pred. No. 7.9e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTGWGYSNTRFTITLNYKDLPTGDE 60
DB 36 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTGWGYSNTRFTITLNYKDLPTGDE 95

QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNQTSMQDEOP 120
DB 96 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNQTSMQDEOP 155

QY 121 SDSFGQAAQSGVWDDSMGLGFSQNFESAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
DB 156 SDSFGQAAQSGVWDDSMGLGFSQNFESAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 215

QY 181 HSLETLYOSADCSDDANDALIIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLOYMH 240
DB 216 HSLETLYOSADCSDDANDALIIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLOYMH 275

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
DB 276 PLCEGSSATLTCVPLGNLIVN----- 297

QY 301 LOKLSRLFKDQVLYPLLAFTROALNLPDVFGVLVPLLEKLRIIFRLLDVRSVLSLSAVCR 360
DB 298 -----ALNLPDVFGVLVPLLEKLRIIFRLLDVRSVLSLSAVCR 335

QY 361 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTKWELRYKRHIQRKESPKGRFVMLLPSSSTH 420
DB 336 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTKWELRYKRHIQRKESPKGRFVMLLPSSSTH 395

QY 421 TIPFYPNPLHPRPFSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCETPSQFPPLRP 480
DB 396 TIPFYPNPLHPRPFSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCETPSQFPPLRP 455

QY 481 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
DB 456 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 497

RESULT 10
US-10-653-595-435
; Sequence 435, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: PZ027PIC1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: FCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 435
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-435

Query Match 87.3%; Score 2404; DB 15; Length 497;
Best Local Similarity 88.1%; Pred. No. 7.9e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTGWGYSNTRFTITLNYKDLPTGDE 60
DB 36 MRLRVLLKRTWPLEVPEPETGLHLRSHLRSLLLCTGWGYSNTRFTITLNYKDLPTGDE 95

QY 61 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNQTSMQDEOP 120
DB 96 ETLASYGIVSGDLICLILODDIPAPNIPSSDSEHSSIQNNEQPSLATSSNQTSMQDEOP 155

QY 121 SDSFGQAAQSGVWDDSMGLGFSQNFESAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
DB 156 SDSFGQAAQSGVWDDSMGLGFSQNFESAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 215

QY 181 HSLETLYOSADCSDDANDALIIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLOYMH 240
DB 216 HSLETLYOSADCSDDANDALIIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLOYMH 275

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
DB 276 PLCEGSSATLTCVPLGNLIVN----- 297

QY 301 LOKLSRLFKDQVLYPLLAFTROALNLPDVFGVLVPLLEKLRIIFRLLDVRSVLSLSAVCR 360
DB 298 -----ALNLPDVFGVLVPLLEKLRIIFRLLDVRSVLSLSAVCR 335

QY 361 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTKWELRYKRHIQRKESPKGRFVMLLPSSSTH 420
DB 336 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTKWELRYKRHIQRKESPKGRFVMLLPSSSTH 395

QY 421 TIPFYPNPLHPRPFSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCETPSQFPPLRP 480
DB 396 TIPFYPNPLHPRPFSSRLPGIIGGEYDQRTPLPYVGDPISSLIIPGCETPSQFPPLRP 455

QY 481 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
DB 456 RFDVPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 497

RESULT 11
US-10-679-246-8
; Sequence 8, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-8

```
Query Match      82.4%; Score 2270; DB 16; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.4e-182;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 92 DSEHSSLNQNEOPSLSATSSNQTSMDQPSDSFQQAQSGVWDDSMLGPSQNFSEESI 151
    |||||
Db 13 DSEHSSLNQNEOPSLSATSSNQTSMDQPSDSFQQAQSGVWDDSMLGPSQNFSEESI 72
    |||||
QY 152 QDNAHMAEGTGFYPSEPMLCSESVEGQVPHSLSTLYQSADCSANDALIVLHLLMLESG 211
    |||||
Db 73 QDNAHMAEGTGFYPSEPMLCSESVEGQVPHSLSTLYQSADCSANDALIVLHLLMLESG 132
    |||||
QY 212 YIPOGTEAKALSMPEKWKLSGVYKLOYMHPLECGSSATLTCVPLGNLIVNATLKINNEI 271
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Db 133 YIPOGTEAKALSMPEKWKLSGVYKLOYMHPLECGSSATLTCVPLGNLIVNATLKINNEI 192
    |||||
QY 272 RVKRLQLLPESFICKEKLGENVANIYKDLQKLSRLFKDQVPLLAFTQALNLPDVFG 331
    |||||
Db 193 RVKRLQLLPESFICKEKLGENVANIYKDLQKLSRLFKDQVPLLAFTQALNLPDVFG 252
    |||||
QY 332 LVVLPLEKLSRLFKDQVPLLAFTQALNLPDVFG 391
    |||||
Db 253 LVVLPLEKLSRLFKDQVPLLAFTQALNLPDVFG 312
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QY 392 WKELYRKHIQKESPKGRFVMLPSSTHTIPFPNPLHPRFPSSRLPPGIIGGEYDQR 451
    |||||
Db 313 WKELYRKHIQKESPKGRFVMLPSSTHTIPFPNPLHPRFPSSRLPPGIIGGEYDQR 372
    |||||
QY 452 PTLVVGDPISLIPGPGTSPQFPLRPDPVGLPGPNLPILGRCGPNDRFPFRSR 511
    |||||
Db 373 PTLVVGDPISLIPGPGTSPQFPLRPDPVGLPGPNLPILGRCGPNDRFPFRSR 432
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QY 512 GRPTDGRLSFM 522
    |||||
Db 433 GRPTDGRLSFM 443
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RESULT 12
US-10-264-237-2484
; Sequence 2484, Application US/10264237
; Publication No. US2004000941A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI31P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2484
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2484

Query Match      55.4%; Score 1527; DB 15; Length 317;
Best Local Similarity 94.0%; Pred. No. 4.3e-120;
Matches 300; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

QY 115 MODEQPSDSFQQAQSGVWDDSMLGPSQNFSEESIQDNAHMAEGTGFYPSEPMLCSES 174
    |||||
Db 1 MODEQPSDSFQQAQSGVWDDSMLGPSQNFSEESIQDNAHMAEGTGFYPSEPMLCSES 60
    |||||
QY 175 VEGQVPHSLSTLYQSADCSANDALIVLHLLMLESGYIPQGTAKALSMPEKWKLSGVY 234
    |||||
Db 61 VEGQVPHSLSTLYQSADCSANDALIVLHLLMLESGYIPQGTAKALSMPEKWKLSGVY 120
    |||||
QY 235 KLOYMHPLECGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKEKLGENV 294
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Db 121 KLOYMHPLECGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKEKLGENV 180
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QY 295 ANIYKDLQKLSRLFKDQVPLLAFTQALNLPDVFGVPLVPLLEKLSRLFKDQVPLVLS 354
    |||||
Db 181 ANIYKDLQKLSRLFKDQVPLLAFTQALNLPDVFGVPLVPLLEKLSRLFKDQVPLVLS 240
    |||||
QY 355 LSACVCRDLFTASNDPMLWRFLYLRDRFRONTVRVQDQTDWKELYRKHIQKESPKGRF--V 412
    |||||
Db 241 LSACVCRDLFTASNDPMLWRFLYLRDRFRONTVRVQDQTDWKELYRKHIQKESPKGRVCD 300
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QY 413 MLLPSSSTHTIPFPNPLHP 431
    |||||
Db 301 PAIVNSHHSI--LSQPLAP 317
    |||||

RESULT 13
US-10-408-765A-752
; Sequence 752, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 752
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-752

Query Match      45.0%; Score 1238; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.7e-96;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 ENVANIYKDLQKLSRLFKDQVPLLAFTQALNLPDVFGVPLVPLLEKLSRLFKDQVPLVLS 351
    |||||
Db 1 ENVANIYKDLQKLSRLFKDQVPLLAFTQALNLPDVFGVPLVPLLEKLSRLFKDQVPLVLS 60
    |||||
QY 352 VLSLSAVCRDLFTASNDPMLWRFLYLRDRFRONTVRVQDQTDWKELYRKHIQKESPKGRF 411
    |||||
Db 61 VLSLSAVCRDLFTASNDPMLWRFLYLRDRFRONTVRVQDQTDWKELYRKHIQKESPKGRF 120
    |||||
QY 412 VMLLPSSSTHTIPFPNPLHP 431
    |||||
Db 121 VMLLPSSSTHTIPFPNPLHP 431
    |||||
QY 472 PSQPPPLRPDPVGLPGPNLPILGRCGPNDRFPFRSRRGPTDGRLSFM 522
    |||||
Db 181 PSQPPPLRPDPVGLPGPNLPILGRCGPNDRFPFRSRRGPTDGRLSFM 231
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RESULT 14
US-10-094-749-1723
; Sequence 1723, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUJI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
```

```
/ APPLICANT: YAMAMOTO, JUN-ICHI
/ APPLICANT: ISONO, YUUKO
/ APPLICANT: HIO, YURI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKA, ICHIRO
/ APPLICANT: SEKI, NAOHIKO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTOKYUKI
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
/ FILE REFERENCE: 084335/0160
/ CURRENT APPLICATION NUMBER: US/10/094,749
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/350,435
/ PRIOR FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: JP 2001-328381
/ PRIOR FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 3381
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1723
/ LENGTH: 221
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-094-749-1723

Query Match      39.4%; Score 1086; DB 15; Length 221;
Best Local Similarity 93.1%; Pred. No. 4.2e-83;
Matches 203; Conservative 4; Mismatches 7; Indels 4; Gaps 1;

QY 309 KDQLVVPILAFTR---QALNLPDVGLVLPLELKLRIFFLLDVRSLVLSAVCRDLFT 364
Db 4 KPDVLYSVIPVTSLFLLALNLPDVGLVLPLELKLRIFFLLDVRSLVLSAVCRDLFT 63

QY 365 ASNDPLLRFLLYLRDRNDTRVQVDTWKELRYKRHIQRKESPKGRFVMLLPSSSTHTTIPF 424
Db 64 ASNDPLLRFLLYLRDRNDTRVQVDTWKELRYKRHIQRKESPKGRFVMLLPSSSTHTTIPF 123

QY 425 YNPLHPRFPSSRLPPGIIIGGEYQRPRTLPLVVGDPISLIPGCGETSPQFPPLPRPDP 484
Db 124 YNPLHPRFPSSRLPPGIIIGGEYQRPRTLPLVVGDPISLIPGCGETSPQFPPLPRPDP 183

QY 485 VGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
Db 184 VGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 221

RESULT 15
US-09-397-945-434
/ Sequence 434, Application US/09397945
/ Publication No. US20030065139A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc. et al.
/ TITLE OF INVENTION: 95 Human secreted proteins
/ FILE REFERENCE: P2027P1
/ CURRENT APPLICATION NUMBER: US/09/397,945
/ CURRENT FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: PCT/US99/05804
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: 60/078,566
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,576
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,573
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,574
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,579
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/080,314
/ PRIOR FILING DATE: 1998-04-01
/
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/ PRIOR APPLICATION NUMBER: 60/080,312
/ PRIOR FILING DATE: 1998-04-01
/ PRIOR APPLICATION NUMBER: 60/078,578
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,581
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,577
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/078,563
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 60/080,313
/ PRIOR FILING DATE: 1998-04-01
/ NUMBER OF SEQ ID NOS: 470
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 434
/ LENGTH: 174
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-397-945-434

Query Match      25.9%; Score 714; DB 10; Length 174;
Best Local Similarity 100.0%; Pred. No. 7.5e-52;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 LYRKRHIQRKESPKGRFVMLLPSSSTHTTIPFYFNPPLHPRFPSSRLPPGIIIGGEYQRPRTL 454
Db 47 LYRKRHIQRKESPKGRFVMLLPSSSTHTTIPFYFNPPLHPRFPSSRLPPGIIIGGEYQRPRTL 106

QY 455 PYVGDPISLIPGCGETSPQFPPLPRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRP 514
Db 107 PYVGDPISLIPGCGETSPQFPPLPRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRP 166

QY 515 TDGRLSFM 522
Db 167 TDGRLSFM 174

Search completed: July 19, 2005, 20:32:50
Job time : 163 secs
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OM protein - protein search, using sw model

Run on: July 19, 2005, 20:13:18 ; Search time 25 Seconds
(without alignments)
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Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MLRLVRLKRTWPLEVPETE.....DRFPFRPSGRPTDGLRSLFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2748	99.8	557	4	US-09-949-016-10867
2	2744	99.6	522	4	US-09-591-694-10
3	2489	90.4	482	4	US-09-385-219A-14
4	2270	82.4	443	4	US-09-591-694-8
5	553	20.1	102	4	US-09-621-976-5935
6	194	7.0	39	4	US-09-385-219A-21
7	189	6.9	38	3	US-09-172-841-47
8	189	6.9	38	4	US-08-951-621-47
9	164	6.0	38	3	US-09-172-841-49
10	164	6.0	38	4	US-08-951-621-49
11	144	5.2	321	4	US-09-166-350-15
12	139	5.0	327	4	US-09-591-694-12
13	139	5.0	327	4	US-09-385-219A-58
14	117.5	4.3	503	4	US-09-599-287A-2
15	117	4.2	507	4	US-09-599-287A-24
16	112	4.1	690	4	US-09-248-796A-19169
17	111.5	4.0	506	4	US-09-949-016-11282
18	111.5	4.0	955	4	US-09-949-016-8369
19	110.5	4.0	553	4	US-09-949-016-7961
20	110	4.0	424	4	US-09-538-092-1338
21	109	4.0	3730	4	US-09-949-016-9908
22	107.5	3.9	776	4	US-09-252-991A-28446
23	107	3.9	78	1	US-08-487-359-5
24	107	3.9	78	1	US-08-222-798A-5
25	107	3.9	489	4	US-09-543-681A-7388
26	107	3.9	557	4	US-09-949-016-7621
27	105	3.8	297	4	US-09-252-991A-29217

28	105	3.8	562	4	US-09-949-016-9186	Sequence 9186, Ap
29	104.5	3.8	850	4	US-09-949-016-11324	Sequence 11324, A
30	104	3.8	1312	4	US-09-554-572-26	Sequence 26, Appl
31	103.5	3.8	79	1	US-08-487-359-8	Sequence 8, Appli
32	103.5	3.8	79	1	US-08-222-798A-8	Sequence 8, Appli
33	103.5	3.8	580	3	US-08-906-865-1	Sequence 1, Appli
34	103.5	3.8	580	4	US-09-129-668-1	Sequence 1, Appli
35	103.5	3.8	888	2	US-08-861-464-6	Sequence 6, Appli
36	103.5	3.8	888	2	US-08-396-001-6	Sequence 6, Appli
37	103.5	3.8	888	3	US-09-323-433A-6	Sequence 6, Appli
38	103.5	3.8	888	4	US-09-826-752-6	Sequence 6, Appli
39	103	3.7	133	4	US-09-252-991A-21490	Sequence 21490, A
40	103	3.7	431	4	US-09-248-796A-17260	Sequence 17260, A
41	102.5	3.7	79	1	US-08-487-359-2	Sequence 2, Appli
42	102.5	3.7	79	1	US-08-222-798A-2	Sequence 2, Appli
43	102.5	3.7	644	4	US-09-198-452A-822	Sequence 822, App
44	102.5	3.7	644	4	US-09-438-185A-774	Sequence 774, App
45	102	3.7	141	4	US-09-270-767-38716	Sequence 38716, A

ALIGNMENTS

RESULT 1
US-09-949-016-10867
; Sequence 10867, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10867
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10867

Query Match	99.8%	Score	2748	DB	4	Length	557
Best Local Similarity	99.8%	Pred. NO.	1.5e-255				
Matches	521	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
Qy	1	MLRLVRLKRTWPLEVPETE	1	MLRLVRLKRTWPLEVPETE	1	MLRLVRLKRTWPLEVPETE	60
Db	36	MLRLVRLKRTWPLEVPETE	36	MLRLVRLKRTWPLEVPETE	36	MLRLVRLKRTWPLEVPETE	95
Qy	61	ETLASYGVSGDLICLI	61	ETLASYGVSGDLICLI	61	ETLASYGVSGDLICLI	120
Db	96	ETLASYGVSGDLICLI	96	ETLASYGVSGDLICLI	96	ETLASYGVSGDLICLI	155
Qy	121	SDSFGQAAQSGVND	121	SDSFGQAAQSGVND	121	SDSFGQAAQSGVND	180
Db	156	SDSFGQAAQSGVND	156	SDSFGQAAQSGVND	156	SDSFGQAAQSGVND	215
Qy	181	HSLETLYOSADCS	181	HSLETLYOSADCS	181	HSLETLYOSADCS	240
Db	216	HSLETLYOSADCS	216	HSLETLYOSADCS	216	HSLETLYOSADCS	275
Qy	241	PLCEGSSATLTCV	241	PLCEGSSATLTCV	241	PLCEGSSATLTCV	300
Db	276	PLCEGSSATLTCV	276	PLCEGSSATLTCV	276	PLCEGSSATLTCV	335
Qy	301	LQKLSRLFKDQIV	301	LQKLSRLFKDQIV	301	LQKLSRLFKDQIV	360

Db 336 LOKLSRLFKDQVLYPLLAFTQALNLPDVFGVLVPLPLELKLRIFRLLDVRSLSAVCR 395
Qy 361 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 420
Db 396 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 455
Qy 421 TTFYFVNPVLPHPFPSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 480
Db 456 TTFYFVNPVLPHPFPSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 515
Qy 481 REDPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
Db 516 REDPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 557

RESULT 2
US-09-591-694-10
; Sequence 10, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Macusawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; EARLIER FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US-09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-10

Query Match 99.6%; Score 2744; DB 4; Length 522;
Best Local Similarity 99.6%; Pred. No. 3.2e-255;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVETPTGLHLSRLSLCTWGYSSNTRFTITLNYKDPITGDE 60
Db 1 MRLRVLLKRTWPLEVETPTGLHLSRLSLCTWGYSSNTRFTITLNYKDPITGDE 60
Qy 61 ETLASGIVSGDLICLILODDIPAPNIPSTDSHSSLQNNQPSLATSSNOTSMQDEQP 120
Db 61 ETLASGIVSGDLICLILODDIPAPNIPSTDSHSSLQNNQPSLATSSNOTSMQDEQP 120
Qy 121 SDSFQQAQSGVWDDSMGLPSONFEAESIODNAHMAEGTFYPSEPMLCSESVEGQVP 180
Db 121 SDSFQQAQSGVWDDSMGLPSONFEAESIODNAHMAEGTFYPSEPMLCSESVEGQVP 180
Qy 181 HSLETLYQSADCSANDALIVLIHLLMLSSGYIPQTEAKALSMPEKWLKSGVYKLYMH 240
Db 181 HSLETLYQSADCSANDALIVLIHLLMLSSGYIPQTEAKALSMPEKWLKSGVYKLYMH 240
Qy 241 PLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLPSPFTCKEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLPSPFTCKEKLGENVANIYKD 300
Qy 301 LOKLSRLFKDQVLYPLLAFTQALNLPDVFGVLVPLPLELKLRIFRLLDVRSLSAVCR 360
Db 301 LOKLSRLFKDQVLYPLLAFTQALNLPDVFGVLVPLPLELKLRIFRLLDVRSLSAVCR 360
Qy 361 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 420
Db 361 DLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHIORKESPKGRFVMLLPSSSTH 420
Qy 421 TTFYFVNPVLPHPFPSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 480
Db 421 TTFYFVNPVLPHPFPSSRLPPGIIGGEYDQRTPLPVVGDPISSLIPGCGTSPQPPPLRP 480

Qy 481 REDPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522
Db 481 REDPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSFM 522

RESULT 3
US-09-385-219A-14
; Sequence 14, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-14

Query Match 90.4%; Score 2489; DB 4; Length 482;
Best Local Similarity 98.1%; Pred. No. 1e-230;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNRTFTITLNYKDPITGDEETLASGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 101
Db 2 SNRTFTITLNYKDPITGDEETLASGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 61
Qy 102 EOPSLATSSNOTSMQDEQPSDSFQQAQSGVWDDSMGLPSONFEAESIODNAHMAEGT 161
Db 62 EOPSLATSSNOTSIQDEQPSDSFQQAQSGVWDDSMGLPSONFEAESIODNAHMAEGT 121
Qy 162 GYPSEPMLCSESVEGQVPHSLETLYQSADCSANDALIVLIHLLMLSSGYIPQTEAKA 221
Db 122 GYPSEPMLCSESVEGQVPHSLETLYQSADCSANDALIVLIHLLMLSSGYIPQTEAKA 181
Qy 222 LSMPEKWLKSGVYKLYMHPLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWLKSGVYKLYMHPLCEGSSATLTCVPLGNLIVVWATLKINNEIRSVKRLQLLP 241
Qy 282 ESFICEKELGENVANIYKDLQKLSRLFKDQVLYPLLAFTQALNLPDVFGVLVPLPLELKL 341
Db 242 ESFICEKELGENVANIYKDLQKLSRLFKDQVLYPLLAFTQALNLPDVFGVLVPLPLELKL 301
Qy 342 RIFRLLDVRSVLISAVCRDLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHI 401
Db 302 RIFRLLDVRSVLISAVCRDLFTASNDPLLWRFLYLRDRFRONTVRVQDQDKELYRKHHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFYPNPLHPFPSSRLPPGIIGGEYDQRTPLPVGDPI 461
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFYPNPLHPFPSSRLPPGIIGGEYDQRTPLPVGDPI 421
Qy 462 SSLIPGCGTSPQPPPLRPFRDPPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
Db 422 SSLIPGCGTSPQPPPLRPFRDPPVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482

RESULT 4

US-09-591-694-8
; Sequence 8, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-8

Query Match 82.4%; Score 2270; DB 4; Length 443;
Best Local Similarity 99.8%; Pred No. 1.1e-209; Mismatches 0; Indels 0; Gaps 0;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 92 DSEHSLQNNQPSLATSSNOTSMQDEQPSDFQQAAGVWDDSMGLPSSQNFEEESI 151
DB 13 DSEHSLQNNQPSLATSSNOTSMQDEQPSDFQQAAGVWDDSMGLPSSQNFEEESI 72
QY 152 QNNAHMAECTGYPSEPMCLCSSEVSGQVPHSLTLYQSDADCDANDALIVLHLLMLSEG 211
DB 73 QNNAHMAECTGYPSEPMCLCSSEVSGQVPHSLTLYQSDADCDANDALIVLHLLMLSEG 132
QY 212 YIPOQTEAKALSMPEKWKLVGYKQYMHPLCEGSSATLTCVPLGNLIVVATLKNNEI 271
DB 133 YIPOQTEAKALSMPEKWKLVGYKQYMHPLCEGSSATLTCVPLGNLIVVATLKNNEI 192
QY 272 RSVKRLQLLPESFICEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVF 331
DB 193 RSVKRLQLLPESFICEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVF 252
QY 332 LVVPLELKLRIFFLLDVRVSVLSAVCRDLFTASNDPLLRFLYLRFRDNTVRVQD 391
DB 253 LVVPLELKLRIFFLLDVRVSVLSAVCRDLFTASNDPLLRFLYLRFRDNTVRVQD 312
QY 392 WKELYRKHIQKESPKGRFVMLLPSSHTTIPFYNPLHPRFPSSRLPPGIIIGGEYDOR 451
DB 313 WKELYRKHIQKESPKGRFVMLLPSSHTTIPFYNPLHPRFPSSRLPPGIIIGGEYDOR 372
QY 452 PTLPVGDPISLIPGPGTTPSQFPPLRPFRFPVGPPLPGPNILPGRGPNDRFPFRPSR 511
DB 373 PTLPVGDPISLIPGPGTTPSQFPPLRPFRFPVGPPLPGPNILPGRGPNDRFPFRPSR 432
QY 512 GRPTDGRLSFM 522
DB 433 GRPTDGRLSFM 443

RESULT 5

US-09-621-976-5935
; Sequence 5935, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm

; SEQ ID NO 5935

; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 87
; OTHER INFORMATION: Xaa = Cys,Gly
US-09-621-976-5935

Query Match 20.1%; Score 553; DB 4; Length 102;
Best Local Similarity 99.0%; Pred No. 2.1e-45;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 413 MLLPSSTHTTIPFYNPLHPRFPSSRLPPGIIIGGEYDQRPRTLPPYVGDPISSLIIPGGETP 472
DB 1 MLLPSSTHTTIPFYNPLHPRFPSSRLPPGIIIGGEYDQRPRTLPPYVGDPISSLIIPGGETP 60
QY 473 SQFPLRFRFPVGPPLPGPNILPGRGPNDRFPFRPSR 511
DB 61 SQFPLRFRFPVGPPLPGPNILPGRGPNDRFPFRPSR 99

RESULT 6

US-09-385-219A-21
; Sequence 21, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match 7.0%; Score 194; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFFLLDVRVSVLSAVCRDLFTASNDPLLR 373
DB 1 LPLEKLRIFFLLDVRVSVLSAVCRDLFTASNDPLLR 39

RESULT 7

US-09-172-841-47
; Sequence 47, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0

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; SEQ ID NO 47
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-841-47

Query Match
Best Local Similarity 6.9%; Score 189; DB 3; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 38

RESULT 8
US-09-951-621-47
; Sequence 47, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-47

Query Match
Best Local Similarity 6.9%; Score 189; DB 4; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 38

RESULT 9
US-09-172-841-49
; Sequence 49, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-841-49

Query Match
Best Local Similarity 6.0%; Score 164; DB 3; Length 38;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 38

RESULT 10
US-08-951-621-49
; Sequence 49, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-49

Query Match
Best Local Similarity 6.0%; Score 164; DB 4; Length 38;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 335 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 372
Db 1 LPLEKLRIFRLLDVRSLSAVCRDLFTASNDPLW 38

RESULT 11
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US-09-166-350-15
; Sequence 15, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-15

Query Match
Best Local Similarity 5.2%; Score 144; DB 4; Length 321;
Matches 74; Conservative 47; Mismatches 90; Indels 110; Gaps 16;

QY 233 VYKLOYMHPCLCG-SATITCVPL-----GNLIVNATLKINNE-----TRSV-- 274
Db 35 MPRQWMPFELAPGVSSNLENPCRAAGSLQKTSADTKGQEQAKEKARELFKAVEE 94
QY 275 -----KRLQLLPE-----SFICKEKLGENVANIY-----KOLQKLSRL---FK 309
Db 95 EQNGALYEAIFYRRAMQLVPDIEKITVTRSPDGGVGNSTIEDNDDSKWADLLSYFO 154
QY 310 DQVLYPLAFTQALNL---PDV-----FGLVYLPLEKLRIFRL-----LDVRSVLSAV 358
Db 155 QQ-----LTFQESVLKLCQPELESSQIHISLPMVLYIFRWVWSSDLDLSLEQLSIV 209
QY 359 CRDLTASNDPLLRFLYLRDRDNTVR-VQTDWKELRYKRHIOKESPKGRFVMLLPS 417
Db 210 CRGFICARDPEIWRACLKVGRCIKLVPTYSWREMPLE-----PRVFDGVYIS 262
QY 418 ST-----HTIPFPNPLHPRPFSSRLPPGIIGGEYDQRTPLPVGDP 460
Db 263 KTYIRQGEQSLDGFYRAWHQVEYY---RYIRFFPDGHV----- 298
QY 461 ISSLIPGGETSPQPPPLRPR 481
Db 299 --MLTTPPEQSIIVRLRTR 317

RESULT 12
US-09-591-694-12
; Sequence 12, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 327
; TYPE: PRT

; ORGANISM: Homo sapien
US-09-591-694-12

Query Match
Best Local Similarity 5.0%; Score 139; DB 4; Length 327;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

QY 291 GENVANIY-----KOLQKLSRL---FKDQLVYPLLAFTQALNL---PDV-----FGLVVLPL 337
Db 19 GDGVGNSYIEDNDDSKWADLLSYFQQ-----LTFQESVLKLCQPELESSQIHISVLEPM 73
QY 338 ELKLRIFRL-----LDVRSVLSAVCRDLFTASNDPLLRFLYLRDRDNTVR-VQD 391
Db 74 EVLYIFRWVWSSDLDLSLEQLSLVCRGFYICARDPEIWRACLKVGRCIKLVPTYS 133
QY 392 WKELYRKHIORKESPKGRFVMLLPSST-----HTIPFPNPLHPRPF 434
Db 134 WREMPLE-----PRVFDGVYISKTYIRQGEQSLDGFYRAWHQVEYY---RYIRFF 183
QY 435 PSSRLPPGIIGGEYDQRTPLPVVGDPISLSLIPGGETSPQPPPLRPR 481
Db 184 PDGHV-----MMLTTPPEQSIIVRLRTR 207

RESULT 13
US-09-385-219A-58
; Sequence 58, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 58
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-58

Query Match
Best Local Similarity 5.0%; Score 139; DB 4; Length 327;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

QY 291 GENVANIY-----KOLQKLSRL---FKDQLVYPLLAFTQALNL---PDV-----FGLVVLPL 337
Db 19 GDGVGNSYIEDNDDSKWADLLSYFQQ-----LTFQESVLKLCQPELESSQIHISVLEPM 73
QY 338 ELKLRIFRL-----LDVRSVLSAVCRDLFTASNDPLLRFLYLRDRDNTVR-VQD 391
Db 74 EVLYIFRWVWSSDLDLSLEQLSLVCRGFYICARDPEIWRACLKVGRCIKLVPTYS 133
QY 392 WKELYRKHIORKESPKGRFVMLLPSST-----HTIPFPNPLHPRPF 434
Db 134 WREMPLE-----PRVFDGVYISKTYIRQGEQSLDGFYRAWHQVEYY---RYIRFF 183
QY 435 PSSRLPPGIIGGEYDQRTPLPVVGDPISLSLIPGGETSPQPPPLRPR 481
Db 184 PDGHV-----MMLTTPPEQSIIVRLRTR 207

RESULT 14
US-09-599-287A-2
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